

Db 301 GTACATCAAGATGGAATGGGGCTAGAGTATCTGTGAACGGTGCAATAACGACCTGTG 360
QY 361 ATTGAGCTGTTTTCTGTGCAAAATGTTTTCAAGCGAATGTTAGTTTTGCGACCCCTTG 420
Db 361 ATTGAGCTGTTTTCTGTGCAAAATGTTTTCAAGCGAATGTTAGTTTTGCGACCCCTTG 420
QY 421 TGGCGCATTTCAACAGTTGAGCGTGCAGAAAGCCGCACTCCGCCATCGCACTAGCCCC 480
Db 421 TGGCGCATTTCAACAGTTGAGCGTGCAGAAAGCCGCACTCCGCCATCGCACTAGCCCC 480
QY 481 GATTGATCTACAGCAATGATGTAAGTGGCGGATGTAAGATTTGGCTGCGAATTTG 540
Db 481 GATTGATCTACAGCAATGATGTAAGTGGCGGATGTAAGATTTGGCTGCGAATTTG 540
QY 541 CGATATTTGCTTTCTTCAGAGTACGTCAACAGTATACCAAGTGCAGTGCAGTGCAGGCT 600
Db 541 CGATATTTGCTTTCTTCAGAGTACGTCAACAGTATACCAAGTGCAGTGCAGGCT 600
QY 601 GACCTCTGCGTATGCGCTGTACTATACGATGTGGAATATCACTGTAATACGATCACAT 660
Db 601 GACCTCTGCGTATGCGCTGTACTATACGATGTGGAATATCACTGTAATACGATCACAT 660
QY 661 CTTCAACCAATCGGTGTGAGAGAGATGCGGCTCAACGTTTTCATGTTGAGGCAA 720
Db 661 CTTCAACCAATCGGTGTGAGAGAGATGCGGCTCAACGTTTTCATGTTGAGGCAA 720
QY 721 GTTGACACCAACTCTTCACAACTGTGAGGTTGACCGTTGATCCGTTCAATTCAGGC 780
Db 721 GTTGACACCAACTCTTCACAACTGTGAGGTTGACCGTTGATCCGTTCAATTCAGGC 780
QY 781 TGGTGCTACCCGCTGAGGTTGCGGAGAAATTCGAGACGATGTGAGCAATGGCCGCG 840
Db 781 TGGTGCTACCCGCTGAGGTTGCGGAGAAATTCGAGACGATGTGAGCAATGGCCGCG 840
QY 841 GTCTTAATGCTTCCCTGTGTGAGGTTGCTGCGGCAATGATGGGTGGCGCTGTGCTGT 900
Db 841 GTCTTAATGCTTCCCTGTGTGAGGTTGCTGCGGCAATGATGGGTGGCGCTGTGCTGT 900
QY 901 GCTGTGAGGTGAGTGGAGGTTTCCCTAATGCTTTTATTAACCGCGTTACAGATCAT 960
Db 901 GCTGTGAGGTGAGTGGAGGTTTCCCTAATGCTTTTATTAACCGCGTTACAGATCAT 960
QY 961 TGCCACGACGTATTTTGGGAGAGAGGTTTGGCTACTTCTTCCAAATGTTGG 1020
Db 961 TGCCACGACGTATTTTGGGAGAGAGGTTTGGCTACTTCTTCCAAATGTTGG 1020
QY 1021 TGGTTTTTGTGCAAGTGGCTGCAATGCTTATCTTGTGCGTGTGCAATTTGCT 1080
Db 1021 TGGTTTTTGTGCAAGTGGCTGCAATGCTTATCTTGTGCGTGTGCAATTTGCT 1080
QY 1081 TGAAGTCAAAACCGACGACGATCATGCAATGGAATGTTGTGCTGTGGAGTTGAC 1140
Db 1081 TGAAGTCAAAACCGACGACGATCATGCAATGGAATGTTGTGCTGTGGAGTTGAC 1140
QY 1141 ACTTGTGCAATCTTCTGAGAGAGGATCAACGGGCGCTCCGATGACAGCAAGTGCAGAT 1200
Db 1141 ACTTGTGCAATCTTCTGAGAGAGGATCAACGGGCGCTCCGATGACAGCAAGTGCAGAT 1200
QY 1201 TTTTGAACACTCGGTTTACCGGCGGCAATGTTGTGCGCGTGGGATTTGGGCAATCACT 1260
Db 1201 TTTTGAACACTCGGTTTACCGGCGGCAATGTTGTGCGCGTGGGATTTGGGCAATCACT 1260
QY 1261 TTTGAAATCTTGATGATGATGTTGCTTGCATGAGTCCGCTGACGACCTTAATTAATTC 1320
Db 1261 TTTGAAATCTTGATGATGATGTTGCTTGCATGAGTCCGCTGACGACCTTAATTAATTC 1320
QY 1321 GTCTAATTCGCGCGGATTAATGCTGTGAGGCTCAACGAGCGGCTTGCAGATGGGTTG 1380
Db 1321 GTCTAATTCGCGCGGATTAATGCTGTGAGGCTCAACGAGCGGCTTGCAGATGGGTTG 1380
QY 1381 TTAACGCGAGTGGTCTCGGTGATTTATTCGAGGCTTAATCGGCTGATGGGTTCTCGTT 1440
Db 1381 TTAACGCGAGTGGTCTCGGTGATTTATTCGAGGCTTAATCGGCTGATGGGTTCTCGTT 1440

QY 1441 TTAATACCTTGTGTTTATTTAGAGCCCGCTCTGCGGCTGCGATTGCTGCAACAGC 1500
Db 1441 TTAATACCTTGTGTTTATTTAGAGCCCGCTCTCTGCGGCTGCGATTGCTGCAACAGC 1500
QY 1501 AGTTGGTTTCACTGATGTTGCTTCCCGCTGATTTCTGATTCACCGTTGATTTGGC 1560
Db 1501 AGTTGGTTTCACTGATGTTGCTTCCCGCTGATTTCTGATTCACCGTTGATTTGGC 1560
QY 1561 GATTGCGGATATCAACCAATGCTTCCAGGTCTAGCAATTTACCGGAAATGATACGCAC 1620
Db 1561 GATTGCGGATATCAACCAATGCTTCCAGGTCTAGCAATTTACCGGAAATGATACGCAC 1620
QY 1621 CTTGAATGATCAAACTCATGAGTTTCAACCAATTTCCGTTGCTTTAGCCACTGCTTC 1680
Db 1621 CTTGAATGATCAAACTCATGAGTTTCAACCAATTTCCGTTGCTTTAGCCACTGCTTC 1680
QY 1681 ATCACTTGCCTGCGCTGTTTGGGTGATGATTTGCGGCAAGCTACGCTGCTCAC 1740
Db 1681 ATCACTTGCCTGCGCTGTTTGGGTGATGATTTGCGGCAAGCTACGCTGCTCAC 1740
QY 1741 ACGTTCAACCCATACCGTGCATTTTACAGAGCAATGATGTTCTCTTCCAGAGAGAGC 1800
Db 1741 ACGTTCAACCCATACCGTGCATTTTACAGAGCAATGATGTTCTCTTCCAGAGAGAGC 1800
QY 1801 TGAGCAGATCAGCGCGGAGAGAAACGTCCAAAGACTAATCAAAATTCGTTAATA 1860
Db 1801 TGAGCAGATCAGCGCGGAGAGAAACGTCCAAAGACTAATCAAAATTCGTTAATA 1860
QY 1861 AAGGTAAATTCACCTGTGATGAGGCTTTCGCTTAAATGCGTTAAGTTGGGTCGA 1920
Db 1861 AAGGTAAATTCACCTGTGATGAGGCTTTCGCTTAAATGCGTTAAGTTGGGTCGA 1920
QY 1921 TCGCTTTTAAACATCGAGAGGATCTTTCGCGGCAAAATACGAGACACTGCTCCACC 1980
Db 1921 TCGCTTTTAAACATCGAGAGGATCTTTCGCGGCAAAATACGAGACACTGCTCCACC 1980
QY 1981 CAGAAATCCCTTCAAGCTGTGTAAGAGAAACGAGCGGTCGCGAGGATTTGTTGCA 2040
Db 1981 CAGAAATCCCTTCAAGCTGTGTAAGAGAAACGAGCGGTCGCGAGGATTTGTTGCA 2040
QY 2041 CCTATTCTAGAGCTTCTTGCACGCGCTCATTTGATGATGATGATGATGATGATGATG 2100
Db 2041 CCTATTCTAGAGCTTCTTGCACGCGCTCATTTGATGATGATGATGATGATGATGATG 2100
QY 2101 AAGGCTGCGTTACCAAGAGTCTTCTGAACAGAGAACTCAGCCAAAGAGGCTA 2160
Db 2101 AAGGCTGCGTTACCAAGAGTCTTCTGAACAGAGAACTCAGCCAAAGAGGCTA 2160
QY 2161 CAAAGCGACTCGTAAGGACCAAGCTAAGAGGCTGCTTAAGAAACGACCAAGAGA 2220
Db 2161 CAAAGCGACTCGTAAGGACCAAGCTAAGAGGCTGCTTAAGAAACGACCAAGAGA 2220
QY 2221 CCACTAAGAAATCTAATAAAGACCAACGCAAAAGACCAAGAAAGTCTTAAGCG 2280
Db 2221 CCACTAAGAAATCTAATAAAGACCAACGCAAAAGACCAAGAAAGTCTTAAGCG 2280
QY 2281 GATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
Db 2281 GATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
QY 2341 TGAAGTCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
Db 2341 TGAAGTCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
QY 2401 GCGTTTCCCGCTTCTGAGAAACATCGGATGATGATGATGATGATGATGATGATGATG 2460
Db 2401 GCGTTTCCCGCTTCTGAGAAACATCGGATGATGATGATGATGATGATGATGATGATG 2460
QY 2461 AAGTTCAACCGCAATTTGCAACAGATACGAGTGTGTTGCTGCAACCTGTTGCTCA 2520
Db 2461 AAGTTCAACCGCAATTTGCAACAGATACGAGTGTGTTGCTGCAACCTGTTGCTCA 2520

QY 2521 CTGCAAGTGAATGAGAGGCTTCTACGAGGAGGCTTTCAACGCAACGCTGTGAGCTCTTT 2580
Db 2521 CTGCAAGTGAATGAGAGGCTTCTACGAGGAGGCTTTCAACGCAACGCTGTGAGCTCTTT 2580
QY 2581 TCCAGATTTGATTTGATCTCTCGGTGTACCAACACCGATTGGTGGCATCGTTTGGGGAAG 2640
Db 2581 TCCAGATTTGATTTGATCTCTCGGTGTACCAACACCGATTGGTGGCATCGTTTGGGGAAG 2640
QY 2641 TAAACCTAAGTTGGCTGAAGCCGTGAGCCAAAGTGGCGCAACAGGTGCCACTGTGTGG 2700
Db 2641 TAAACCTAAGTTGGCTGAAGCCGTGAGCCAAAGTGGCGCAACAGGTGCCACTGTGTGG 2700
QY 2701 TGCAGGATATCAGCTGTGTGTGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2760
Db 2701 TGCAGGATATCAGCTGTGTGTGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2760
QY 2761 AGATCGGTTTCTCTCCACATCCGCTTCCCTCCCGGATCTGTGCTGTGCTGTGCTGTG 2817
Db 2761 AGATCGGTTTCTCTCCACATCCGCTTCCCTCCCGGATCTGTGCTGTGCTGTGCTGTG 2817

RESULT 2
US-09-431-099-3
Sequence 3, Application US/09431099
Patent No. 6410705
GENERAL INFORMATION:
APPLICANT: Degussa-Höls AG
APPLICANT: Forchungszenentrum-Joachim GmbH
TITLE OF INVENTION: New nucleotide sequences coding for the thrE gene and process for
FILE REFERENCE: 990079 BT
CURRENT APPLICATION NUMBER: US/09/431, 099
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 1909
TYPE: DNA
ORGANISM: Corynebacterium glutamicum ATCC13032
FEATURE:
NAME/KEY: CDS
LOCATION: (280) ..(1746)
OTHER INFORMATION: thrE-Gen
US-09-431-099-3

Query Match 65.2%; Score 1836.6; DB 4; Length 1909;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 156 CCCCTTTGACCTGTGTATTTAGCTGGAGAGAGACTTGAACCTTCAACCTAAGCATTA 215
Db 38 CCCCTTTGACCTGTGTATTTAGCTGGAGAGAGACTTGAACCTTCAACCTAAGCATTA 97
QY 216 CAAGTGGTGGCTGCAATTTGGCCATCCGAGCCGAGAGTGTGATGATCAACAC 275
Db 98 CAAGTGGTGGCTGCAATTTGGCCATCCGAGCCGAGAGTGTGATGATCAACAC 157
QY 276 TACGAATACGATCTTACGATATGTATCATCAATGAGATTCGGGGCTAAGATCTG 335
Db 158 TACGAATACGATCTTACGATATGTATCATCAATGAGATTCGGGGCTAAGATCTG 217
QY 336 GTGAACCGTGCATAACGACCTGTGATTTGATCTTTTCTTGGCAAAATGTTTCCAGC 395
Db 218 GTGAACCGTGCATAACGACCTGTGATTTGATCTTTTCTTGGCAAAATGTTTCCAGC 277
QY 396 GGATGTTGAGTTTGGAGCCCTTGTGGCGCATTTCAACAGTGAAGTGGCAAAAGCCG 455
Db 278 GGATGTTGAGTTTGGAGCCCTTGTGGCGCATTTCAACAGTGAAGTGGCAAAAGCCG 337
QY 456 CACCTTCGCGCATGCGCATGAGCCCGGATTTGATCTCACTGACATAGTCAAGTGGCCGCTG 515
Db 338 CACCTTCGCGCATGCGCATGAGCCCGGATTTGATCTCACTGACATAGTCAAGTGGCCGCTG 397

QY 516 TGATGAATTTGGCTGCGAGAAATGGCGATATTTGCTTCTTCAAGTACGTCAACAGTGG 575
Db 398 TGATGAATTTGGCTGCGAGAAATGGCGATATTTGCTTCTTCAAGTACGTCAACAGTGG 457
QY 576 ATACCAAGTGGCAAGTTGAGCGGTGACCTGTGCGATATGAGCTGTACTATAAGCATGTGG 635
Db 458 ACACCAAGTGGCAAGTTGAGCGGTGACCTGTGCGATATGAGCTGTACTATAAGCATGTGG 517
QY 636 ATATCAGTGAATACGATACCATCTTACCAACATGTGTGTGAGAGGAGATGCTGG 695
Db 518 ATATCAGTGAATACGATACCATCTTACCAACATGTGTGTGAGAGGAGATGCTGG 577
QY 696 TCAACGTTTTCATGTTGGGCAAGTTGACACCAACTTCCAAACCTGCTGAGGTTG 755
Db 578 TCAACGTTTTCATGTTGGGCAAGTTGAGACCAACTTCCAAACCTGCTGAGGTTG 637
QY 756 ACCGTTGATCCGTTCCATTCAGGCTGTGTGCTACCCCGCTGAGGTGCGGAAATTC 815
Db 638 ACCGTTGATCCGTTCCATTCAGGCTGTGTGCTACCCCGCTGAGGTGCGGAAATTC 697
QY 816 TGAAGGATGGAGCAATCGCTGCGCTTATAGTTTCCCTGCTGCTGTGCTGCTGCTG 875
Db 698 TGAAGGATGGAGCAATCGCTGCGCTTATAGTTTCCCTGCTGCTGTGCTGCTGCTG 757
QY 876 CAATGATGGTGGCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 935
Db 758 CAATGATGGTGGCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 817
QY 936 CTTTATTTACCGGTTTACGATATTTGCAACGAGTCAATTTTGGGAAAGAGGTTTGC 995
Db 818 CTTTATTTACCGGTTTACGATATTTGCAACGAGTCAATTTTGGGAAAGAGGTTTGC 877
QY 996 CTACTTCTTCCAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1055
Db 878 CTACTTCTTCCAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 937
QY 1056 ATTCTTGGCGTTGCAATTTGTCTTGAATCAACCGAGCCGAGATGATGATCGATG 1115
Db 938 ATTCTTGGCGTTGCAATTTGTCTTGAATCAACCGAGCCGAGATGATGATCGATG 997
QY 1116 TTGTGTGCTGTGTGAGGTTTGAACCTTGTGCAATCTGTGCAAGAGGATCAACGAG 1175
Db 998 TTGTGTGCTGTGTGAGGTTTGAACCTTGTGCAATCTGTGCAAGAGGATCAACGAG 1057
QY 1176 CTCGGTGAACGAGATGACGATTTTGTGAACATCTCTGTTTACCGGCGGATTTGTG 1235
Db 1058 CTCGGTGAACGAGATGACGATTTTGTGAACATCTCTGTTTACCGGCGGATTTGTG 1117
QY 1236 CTGGCGTGGGTTTGGCATTCAGCTTCTGAATCTTGTGATGATGATGATGATGATG 1295
Db 1118 CTGGCGTGGGTTTGGCATTCAGCTTCTGAATCTTGTGATGATGATGATGATGATG 1177
QY 1296 AGTCCGCTGACGACCTAATTTATGCTTACATTTGCGCGCATTTATGCTGTGAGGCTCA 1355
Db 1178 AGTCCGCTGACGACCTAATTTATGCTTACATTTGCGCGCATTTATGCTGTGAGGCTCA 1237
QY 1356 CCGAGCGGCTTTCGAGAGGTTTGAACCGGAGAGTGTCTCGGATATTTAGCGGAGC 1415
Db 1238 CCGAGCGGCTTTCGAGAGGTTTGAACCGGAGAGTGTCTCGGATATTTAGCGGAGC 1297
QY 1416 TTAATGCGGTAGAGGTTTCTGAGTTTATTAATCTTCTGTTTATTTAAGCCCGTCT 1475
Db 1298 TTAATGCGGTAGAGGTTTCTGAGTTTATTAATCTTCTGTTTATTTAAGCCCGTCT 1357
QY 1476 CTGCGGCTGCGATGCTGTGCAACGAGTGTGTTTCACTGAGTGTGCTTGGCCGTGAT 1535
Db 1358 CTGCGGCTGCGATGCTGTGCAACGAGTGTGTTTCACTGAGTGTGCTTGGCCGTGAT 1417
QY 1536 TCTGATTTCCACGTTGATTTGAGGATTTGCGGAGTCAACCAATGCTTCCAGGCTGAG 1595
Db 1418 TCTGATTTCCACGTTGATTTGAGGATTTGCGGAGTCAACCAATGCTTCCAGGCTGAG 1477
QY 1596 CAATTTACCGGAAATGTAAGCCACCTTGAATGATCAACACTCATGAGGTTTCAACCA 1655

Db 1478 CAATTATACCGGAAATGTACGCAACCTGATGATCAAACTCTATGGGTTTCAACACAA 1537
1566 TTGCGGTTGCTTAAAGCACTGCTTATCATCTTGGCGCTGGCGTGGTTTGGGTAGTGA 1715
Db 1538 TTGCGGTTGCTTAAAGCACTGCTTATCATCTTGGCGCTGGCGTGGTTTGGGTAGTGA 1597
Qy 1716 TTGCGGCGAGGCTTAAAGCACTGCTTATCATCTTGGCGCTGGCGTGGTTTGGGTAGTGA 1775
Db 1598 TTGCGGCGAGGCTTAAAGCACTGCTTATCATCTTGGCGCTGGCGTGGTTTGGGTAGTGA 1657
Qy 1776 ATGAGTCTCTCTTCAAG 1835
Db 1658 ATGAGTCTCTCTTCAAG 1717
Qy 1836 AGACTATCAAG 1895
Db 1718 AGACTATCAAG 1777
Qy 1896 TAAATAGCGTGAATATGCGGTGATGCTTTTAAACATCAGAGAGATCTTGGCGCT 1955
Db 1778 TAAATAGCGTGAATATGCGGTGATGCTTTTAAACATCAGAGAGATCTTGGCGCT 1837
Qy 1956 AAAATCAGGACATCGCTCCCAACCCCAAGATCCCTTCAAGCTTTGAAGAGAGAGAGAG 2015
Db 1838 AAAATCAGGACATCGCTCCCAACCCCAAGATCCCTTCAAGCTTTGAAGAGAGAGAGAG 1897
Qy 2016 GCCGGTG 2022
Db 1898 GCCGGTG 1904

RESULT 3

US-09-103-840A-2

Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 5.6%; Score 157.8; DB 3; Length 4403765;
Best Local Similarity 58.2%; Pred. No. 1.8e-38;
Matches 310; Conservative 0; Mismatches 202; Indels 21; Gaps 1;

Qy 2306 CTTTGTAGTTGTTGCTTAAACCGTCTGCAATGATATGATCTGTCCACCCAGATGTAAGTA 2365
Db 3902073 CTTTGTAGTTGTTGCTTAAACCGTCTGCAATGATATGATCTGTGTCCAGAGGACAC 3902132
Qy 2366 TAGCATCTCCCGAGCCCGGAGGCTTGTCAAGGAGGCTTTCCCGGTTCTGAAACAA 2425
Db 3902133 AACCTGGAAG 3902192
Qy 2426 TCGTGAATGTTGGTGTGATGAGCTTGAACCTGATGTTGACACCCGAACATTTTGAAC 2485
Db 3902193 GCGGCGGAGCTGGGTGCTGGGCTGGGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3902252

Qy 2486 AGATAGGGGNG-----TTTGTGACACCTTGTGCTCACTGC 2524
Db 3902253 CTTGTGAG 3902312
Qy 2525 AAGTACTATGAAGGCTTCTAG 2584
Db 3902313 CAGGACATAGCTCAGTACTAG 3902372
Qy 2585 CGATTGATTTGTTACTCGGTTGATCAACACCGATGTTGTCAGTCTGTTGAGAGAGAGAG 2644
Db 3902373 CGAGTATGCTCAAG 3902432
Qy 2645 CCTCAAGTTCGCTGAAG 2704
Db 3902433 CAGAGCTTTGCGAG 3902492
Qy 2705 GACTATCAGCTGTTGTTGCTGCTGAGATTTTGGCGCAAGATGCGCTGATTTGAAGAT 2764
Db 3902493 GACTATCAGCTGTTGTTGCTGCTGAGATTTTGGCGCAAGATGCGCTGAGATTC 3902552
Qy 2765 CGTTTCTTCTCCACATTCCTTCCCTTCCCTGATCTGTTCCGTGAGCTGC 2817
Db 3902553 CGTTTCTTCTTTCGACATTCCTTCCCTTCCCTGATCTGTTTCGATGATGC 3902605

RESULT 4

US-09-103-840A-1

Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 5.6%; Score 157.8; DB 3; Length 4411529;
Best Local Similarity 58.2%; Pred. No. 1.8e-38;
Matches 310; Conservative 0; Mismatches 202; Indels 21; Gaps 1;

Qy 2306 CTTTGTAGTTGTTGCTTAAACCGTCTGCAATGATATGATCTGTCCACCCAGATGTAAGTA 2365
Db 3908294 CTTTGTAGTTGTTGCTTAAACCGTCTGCAATGATATGATCTGTGTCCAGAGGACAC 3908353
Qy 2366 TAGCATCTCCCGAGCCCGGAGGCTTGTCAAGGAGGCTTTCCCGGTTCTGAAACAA 2425
Db 3908354 AACCTGGAAG 3908413
Qy 2426 TCGTGAATGTTGGTGTGATGAGCTTGAACCTGATGTTGACACCCGAACATTTTGAAC 2485
Db 3908414 GCGGCGGAGCTGGGTGCTGGGCTGGGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3908473
Qy 2486 AATATAGGGTG-----TTTGTGACACCTTGTGCTCACTGC 2524
Db 3908474 CTTGTGAG 3908533
Qy 2525 AAGTACTATGAAGGCTTCTAG 2584
Db 3908534 CAGGACATAGCTCAGTACTAG 3908593

QY 2585 CGATTGATTTACTCCGGTGTACACACCGAATTGGTGCATGCGTTTCGGGAAGTAA 2644
Db 390854 CGACGTATCTGTAACCGCTCTTACACCGGAATGGTGGATCTGTAAGTCA 390853
QY 2645 CCTCAAGTTCGCTGAAGCCGTGAGCCAAATGCGCGCACACGATGCACTGATGGGTCGA 2704
Db 390864 CCAGCGCTTTGGCCGAGCGCGGTGCGCGCGCCGCCCAACCGGATGGGATCA 3908713
QY 2705 GGACTATAGCTGTGTGCTGCTGCGCATTTTGGCCGAGATGCGCCCTGATTGGAAGAT 2764
Db 3908714 GGACTACAGCTGACGCTGTACCGAAGATGCTGCGCATGCTGCGGCGCCGATCTGACCAT 3908773
QY 2765 CGGTTCTTCCTCCACATTCCTCCCTCCCTGATGTTTCCGTACGCTGC 2817
Db 3908774 CGGTTCTTTTGGACATCCGCTTCGCGCGGTAGAGCTGTTATGACGATGC 3908826

RESULT 5
US-08-311-731A-136
Sequence 136, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 36138 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mycobacterium leprae
US-08-311-731A-136

Query Match 5.3%; Score 149.4; DB 4; Length 36138;
Best Local Similarity 57.1%; Pred. No. 2.4e-37;
Matches 301; Conservative 0; Mismatches 211; Indels 15; Gaps 1;

QY 2306 CTTTGAAGTGTGTGTAACCGCTTCGACGATGATGACTGTCACCCAGATGATGCTA 2365
Db 27896 CTTTGAAGTGTGTGTAACCGCTTCGACGATGATGACTGTCACCCAGATGATGCTA 27955
QY 2366 TAGCATCTCCCGACCCCGCGTGGCTTGTCAAGGGGCTTTCCCGCTTGTGAACACAA 2425

Db 27956 GATCTGGAAGCGCAGTCCAGCGGGTGTGTACACCGCTTAAGCCGCTGCTGCTACCG 28015
QY 2426 TCGTGATGTTGGGTCCGATGCTCGAACCTGATGATGTTGACCCGACATTTGCAAC 2485
Db 28016 GCGGCGGGCCCTGGGTCCGCTGGCGGGCGGTATTAACGACAAAGTGAACCTGCACTTAC 28075
QY 2486 AGATACG-----GGTGTGTCGACACCTTGTGTCTCATCTGCAAGTGA 2530
Db 28076 CATCAAGTCATCTGACGATGAGCTTACTCTTATCCGATGACGCTGAACACACATGA 28135
QY 2531 CTATGAAGGCTTTACAGAGGCTTTTCAAAAGCAAGCTGAGGCTCTTTTCCAGATTT 2590
Db 28136 TGTGCGGAGTACTACAGAGGCTTCTGAAAGCCACGCTGAGCGCTATACCAAGAGCT 28195
QY 2591 GATTGTACTCCGCTGACACACCGATGATGATGATGATGATGATGATGATGATGATGAT 2650
Db 28196 CATGTAAAGCCCATTTTACACATGCGAATGATGATGATGATGATGATGATGATGATGAT 28255
QY 2651 GTTGTGAAGCGGTGAGCCAAAGTGGGCGACACAGGCTGATGATGATGATGATGATGATGAT 2710
Db 28256 CTTGCGGAAACAAAGCTACACGACGCGCTACGATGATGATGATGATGATGATGATGATGAT 28315
QY 2711 TGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2770
Db 28316 CCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 28375
QY 2771 CTTGCTGACATTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 2817
Db 28376 CTTGCTGACATTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 28422

RESULT 6
US-09-214-808-1
Sequence 1, Application US/09214808A
Patent No. 6475793
GENERAL INFORMATION:
APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
Patent No. 6475793
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARP0068
CURRENT APPLICATION NUMBER: US/09/214,808A
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: PCT/IB97/00950
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 536165
TYPE: DNA
ORGANISM: Rhizobium
US-09-214-808-1

Query Match 2.6%; Score 72.2; DB 4; Length 536165;
Best Local Similarity 52.5%; Pred. No. 8e-11;
Matches 158; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 2517 CTCACGTGCAAGTATGATGAAGGCTTTCAAGAGGCTTTTCAAGCAAGCGTGGGCTT 2576
Db 317398 CTGACCGATACGAGATGATGAAGAAATACACACGCTTCGCAACCGGCTTCTTGCGCG 317457
QY 2577 CTTTTCACGATTTATTTATTTATCTCGGTGTAACAACCGATGATGATGATGATGATGAT 2636
Db 317458 ATTTCGCACTACCGGCTTATCTCGGCAATACCGTTCACAGAAATAGCCGGTATTTTC 317517
QY 2637 GAAATTAACCTCAAGTTCGCTGAAGCGGTGAGCCAAAGTGGGCGACACAGTGGCCACTG 2696
Db 317518 CGGCTCAACCGCTTCTTGGCCCATGCGCTGGCGCGCTTGTCAACCGGATGACGTCAAT 317577

REFERENCE/DOCKET NUMBER: CGNE 86(1)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2868 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-274-121B-1

Query Match 2.5%; Score 71.6; DB 3; Length 2868;
Best Local Similarity 49.1%; Pred. No. 2e-12;
Matches 222; Conservative 0; Mismatches 224; Indels 6; Gaps 1;

2372 CTCCCGCAGCCCGGCTGCTGTCAGGGGCTTCCCGCTTGGAAACAACATCGTG 2431
1500 CGCGCCAGAGCGCGTGGCTTGGCATCTGGGGGCACTGAAAGCCGACGGCGG 1559
2432 ATGTGGGTCGATGGCCTGGAATGATGTTGCAACCCGACATTTGGAACAGATAC 2491
1560 ACTGTGGTTGGCTGAGTGGTGAACAGGGAATGAGGATGACGGCTAAAGGTGA 1619
2492 GGGTG-----TTTGTGTCACCTGTGTCTTACTGCAAGTACTATGAGGCTTCTA 2545
1620 AAAAGTAACTTACGTGGGCTCTTTTAACTTCAGCAACAGACCTTGAACGATCTA 1679
2546 CGAGGGCTTTTCAACGCAACGCTGGGCTCTTTTCCAGATTTGATTTACTCGGT 2605
1680 CAACCAATTCCTCAATGCCCTTCTCTGGCCCGCTTTTCAATTTGCGCTGATCGTGA 1739
2606 GTACACACCGATGTGTGTCATGCTTTCGGGAAGTAACTCAAGTTGCTGAAGCGT 2665
1740 ATTTCAGCGTCTGCTGCGGACGCGCTATCTACGGTAAATGCGTGTGGCAATTAAT 1799
2666 GAGCCAGTGGCGGACACGGTGCCTGCTGTGGTGGTGCAGGATATGAGTGTGTGCTGT 2725
1800 ACTGCGGCTTTGCAAGACGATGACATATATCTGATTCAGATATCACTGTGGCATT 1859
2726 TCTGCGATTTTGGCGCAGATGGCCCTGATTTGAGATGCTTTCTTCCCTCCACATTC 2785
1860 TGGCATGATTTACGAAACGGGAGTGAATATCCGATTTGTTCTTGTGATATTC 1919
2786 CTTCCTTCCCTGATCTGTTCGTGAGCTGC 2817
1920 TTTCGCCAGACCGGAATCTTCAACGCGCTGC 1951

RESULT 9
US-09-489-039A-7037
Sequence 7037, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7037
LENGTH: 1479
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7037

Query Match 2.5%; Score 70.2; DB 4; Length 1479;
Best Local Similarity 52.6%; Pred. No. 3.4e-12;
Matches 153; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

2516 CCTACTGCAAGTACTATGAAGGCTTCTACAGGGCTTTTCAACGCAACGCTGTGGCC 2575
DB CTTATATGAAGGAGCATGATGATTAATTAACCAAGTCTCTTAACGCGCTGTGGCC 314
2576 TCTTTCCAGATTTGATTTGTTACTCGGTGTACAAACCGATTTGATGATGCTTTCG 2635
DB GAGTTCCATATGAGCTTGTATCTGTGAGCTTTTCAAGCGGAGAGCTGGAGGATATCT 374
2636 GGAATTAACCTCAAGTTCGTGAAGCGGTGAGCCAAAGTGCAGGACAGGTCGACATGT 2695
DB GGGGTTTACGCGCATGCTGGCGGCAAGCTTCTCGCTGATTTGACGACAGATACCT 434
2696 GTGGGTGAGACATATGAGCTGTGCTGCTGCTTCCGATTTTGGCCAGATGCGCTTGA 2755
DB GTGATTCATATGATTAATCATCTTCTGCGCTTTCGACGAGCTGTGCAACGCGGGTGA 494
2756 TTGAAAGATCGGTTCTTCTCCACATTTCCCTTCCCTGATCTGTT 2806
DB CAATCGCATCGGGTTTCTTACATATTCGTTCCGACGCGGAGATTTT 545

RESULT 10
US-09-328-352-595
Sequence 595, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 595
LENGTH: 1455
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-595

Query Match 2.0%; Score 56; DB 4; Length 1455;
Best Local Similarity 49.7%; Pred. No. 1.7e-07;
Matches 143; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

2530 ACTAGAAGGCTTTCTACGAGGCTTTTCAACGCAACGCTGTGGCTTTTCAACGATT 2589
DB AATATGACAGTACTACTGTGTTTGGCAATTAAGTATATATGCTGCGCATGATGATC 301
2590 TGAATGTACTCCGCTGTACAAACCGATTTGGTGGCATGCGTTTCGGAAGTAACTCA 2649
DB GGGATGACCTGATGCAATTAATATGAGAAGATATATACCTACAAAAGTCAATGCTT 361
2650 AGTTGCTGAAGCGGTGAGCCAAAGTGGCGGACACGCTGCCACTGTGTGGGTGACAGCT 2709
DB TATTGCTGAAAATAATTAACAAGATTTGCTCACTGATGATCTGATTTGGGTGACATGACT 421
2710 ATCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2769
DB ATCATTCTTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
2770 TCTTCTCCACATTCCTTCCCTTCCCTGATCTGTTCGTGAGCTGC 2817
DB TCTTTTGCATATCTCTTTCGCAAGCTTAATATCTGGGCAAGATCC 529

RESULT 11
US-09-651-169A-36
Sequence 36, Application US/09651169A
Patent No. 6506565
GENERAL INFORMATION:
APPLICANT: Comer, Timothy W
TITLE OF INVENTION: Plant Regulatory Sequences for Selective Control of Gene Expressi

FILE REFERENCE: 06009.00119.NPUS00 (RENN:0109)
CURRENT APPLICATION NUMBER: US/09/651.169A
CURRENT FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.0
SEQ ID NO 36
LENGTH: 654
TYPE: DNA
ORGANISM: Zea mays
US-09-651-169A-36

	Query Match	1.7%	Score 48;	DB 4;	Length 654;	
	Best Local Similarity	51.4%	Pred. No. 4e-05;			
	Matches 108;	Conservative	1;	Mismatches 101;	Indels 0;	Gaps 0;
QY	2608	ACAAACCGATTGTGTGGCATGCGTTTCGGGAAGTAACCTCAAGTTCGCTGAAGCCGCGA	2665			
Db	359	ACCCACAGCGCTTGGAGAGCGATACGTGCTCCGCCACAAAGTTCTTCTTGAGAAGGCTGTGCG	418			
QY	2668	GCCAAAGTGGCGGACACAGGTGCACATGTGTGGGTGCAGAACTATACGCTGTTCGTGCTTC	2722			
Db	419	AGGTAATACCCGGAGSAGATGACTACGTTTGGGTTCAGAGACTACATCTCAAGCGGCTGC	478			
QY	2728	CTGGCAATTTGGCGCCAGATGGCGCCTGTATTGAAATAGGTTTCTTCTCCGACATTCCT	2785			
Db	479	CTACTTCTCTCGCGCGCTTTCACACGCGCTCCGATCGAGATTCTTCTCCACACACCCCT	538			
QY	2788	TCCCTTCCCTGCATCTGTTCCTGCACGTGC	2817			
Db	539	TCCCTTCGTCGAGATCTACCGCACCTTCC	568			

RESULT 12
US-08-232-463-14
; Sequence 14, Application US/08232463

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; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
;
US-08-232-463-14

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Query Match	1.7%;	Score 47.6;	DB 1;	Length 7218;
Best Local Similarity	3.6%;	Pred. No. 0.00037;		
Matches 14;	Conservative 218;	Mismatches 162;	Indels 0;	Gaps 0;

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Qy      1175  GCTCCGGTGCAGCAGAGTGCACATTTTGGAAACACTCCCTGTTACCGCGGCATTGTT 1234
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1042  GCTCCAGGTGCAGGAGACTTGCCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1101

Qy      1235  GCTGCGCGTGAGTTGGGCATTCACGCTTCTGAAATCTTGACATGTCATGTTGCCATG 1294
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1102  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1161

Qy      1295  GAGTCCGCTGCAGCACCTTAATTATTCGTACATTCGCCCGCATTCAGCGTGCAGCTC 1354
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1162  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1221
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      1355  ACCGACGCGCGCTCGCAGTGGTGTGTACCGGAGTGCCTCGGTATTATTCGCGGG 1414
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1222  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1281
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      1415  CTTACTCGCGTCGATGAGGTTCTGCGCTTTATTACTCTTCGTGTTATTAGGCCCGCTC 1474
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1282  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1341
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      1475  TCTGCCGCTGCGATTGCTGCACAAGCAAGTGGTTCACTGGGCTGTTGCTGACCGCTGA 1534
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1342  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1401
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      1535  TTCTGATTCACACGTTGATTTGTGCGAATTGCGG 1568
         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1402  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1435

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RESULT 13
US-09-198-452A-1
; Sequence 1, Application US/09198452A

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? GENERAL INFORMATION:
? APPLICANT: Griffiths, R.
? TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
? TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
? TITLE OF INVENTION: and treatment of infection
? FILE REFERENCE: 9710-003-999
? CURRENT APPLICATION NUMBER: US/09/198,452A
? CURRENT FILING DATE: 1998-11-24
? NUMBER OF SEQ ID NOS: 6849
? SEQ ID NO 1
? LENGTH: 1230025
? TYPE: DNA
? ORGANISM: Chlamydia pneumoniae
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)..(15000)
? OTHER INFORMATION: n=a or c or g or t
? NAME/KEY: misc_feature
? LOCATION: (15001)..(30000)
? OTHER INFORMATION: n=a or c or g or t
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? OTHER INFORMATION: n=a or c or g or t
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? LOCATION: (45001)..(60000)
? OTHER INFORMATION: n=a or c or g or t
? NAME/KEY: misc_feature
? LOCATION: (60001)..(75000)

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LOCATION: (795001)..(810000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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LOCATION: (885001)..(900000)
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NAME/KEY: misc feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature

Query Match 1.6%; Score 45.8; DB 4; Length 1230025;
Best Local Similarity 76.7%; Pred. No. 0.087;
Matches 56; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 179 GCTGAGAGAGACTGTAAGTCTCAAGCTAGCATTAAGTGGCTGGCAATTG 238
DB 303710 GCTGAGAGAGAAATGAACCTCAACCTTGATTAAGTGAATGCTGCGCAATTG 303769

QY 239 CGCCACTCCAGCA 251
DB 303770 AGCTACTCCAGCA 303782

RESULT 14
US-08-956-171E-4023
; Sequence 4023, Application US/08956171E
; Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4023:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4023:
US-08-956-171E-4023

Query Match 1.6%; Score 45.6; DB 4; Length 381;
Best Local Similarity 73.1%; Pred. No. 0.00016;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 174 ATTGAGCTGAGAGAGACTGTAAGTCTCAAGCTAGCATTAAGTGGCTGGCC 233
DB 87 ATGAGCGAGCCAGAGAGACTGAACCCCAAGCTAGTATTAAGTCAAGTGGCTGACC 146

QY 234 AATGGCCCACTCCAGCA 251
DB 147 AATTGAGCTAGGCCGCA 164

RESULT 15
US-08-956-171E-4234/C
; Sequence 4234, Application US/08956171E
; Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4234:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid


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; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4234:
US-08-956-171E-4234

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Query Match      1.6%; Score 44.8; DB 4; Length 400;
Best Local Similarity 61.9%; Pred No.0.00031;
Matches 70; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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OY 215 ACAAGTGGCTGCGCTGCCAATTGGCCACTGCCACCGCAGATGCTGATGA 267
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Db 233 ACAAGTCAAGTTCCTTACCAATTGAGCTAGCGCGCTAAGAAATGTTCAAGGA 181
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Search completed: July 31, 2004, 04:52:18
Job time : 220.085 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 04:42:15 ; Search time 1213.59 Seconds

(without alignments)
11381.257 Million cell updates/sec

Title: US-09-963-521-1

Perfect score: 2817

Sequence: 1 aatgaataatccccctacc.....tgatctgtccgcagctgc 2817

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 3222919 segs, 2451570024 residues 6445838

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%

Maximum March 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2817	100.0	2817	9	US-09-951-536-1 Sequence 1, Appli
2	2817	100.0	2817	9	US-09-963-521-1 Sequence 1, Appli
3	2817	100.0	2817	9	US-09-834-721-1 Sequence 1, Appli
4	2817	100.0	2817	9	US-09-783-388-1 Sequence 1, Appli
5	2817	100.0	2817	10	US-09-951-535-1 Sequence 1, Appli
6	2817	100.0	2817	17	US-10-224-574-9 Sequence 1, Appli
7	2783.4	98.8	3309400	9	US-09-738-626-1 Sequence 1, Appli
8	1836.6	65.2	1909	9	US-09-951-536-1 Sequence 3, Appli
9	1836.6	65.2	1909	9	US-09-963-521-3 Sequence 3, Appli
10	1836.6	65.2	1909	9	US-09-834-721-3 Sequence 3, Appli
11	1836.6	65.2	1909	9	US-09-783-388-3 Sequence 3, Appli
12	1836.6	65.2	1909	10	US-09-951-535-3 Sequence 3, Appli
13	1836.6	65.2	1909	17	US-10-224-574-11 Sequence 11, Appli
14	1561.2	55.4	1590	13	US-10-627-476-557 Sequence 557, App

15	1561.2	55.4	1590	13	US-10-450-055-41	Sequence 41, Appli
16	1474.2	52.3	1503	9	US-09-738-626-2884	Sequence 2884, Ap
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18	969.6	34.4	2369	9	US-09-895-382-29	Sequence 29, Appli
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ALIGNMENTS

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US-09-951-536-1
Sequence 1, Application US/09951536
Patent No. US20020107378A1
GENERAL INFORMATION:
APPLICANT: ZIEGLER, PETRA
APPLICANT: EGGLING, LOTMAR
APPLICANT: SAHM, HERMANN
APPLICANT: THIERBACH, GEORG
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
TITLE OF INVENTION: USING CORNEFORM BACTERIA
FILE REFERENCE: 21123/282414/MAS
CURRENT APPLICATION NUMBER: US/09/951,536
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/431,099
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2817
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (398)..(1864)
OTHER INFORMATION: three-Gen
US-09-951-536-1

Query Match 100.0%; Score 2817; DB 9; Length 2817;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-834-721-1
Sequence 1, Application US/09834721
Patent No. US2002015551A1
GENERAL INFORMATION:
APPLICANT: RIEPING, MECHTILD
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
FILE REFERENCE: 21123/280169/MAS
CURRENT APPLICATION NUMBER: US/09/834,721
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: DE 100 26 494.8
PRIOR FILING DATE: 2000-05-27
PRIOR APPLICATION NUMBER: DE 101 02 823.7
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2817
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
OTHER INFORMATION: ATCC14752
NAME/KEY: CPS
LOCATION: (398). (1864)
OTHER INFORMATION: three gene
US-09-834-721-1

Query Match 100.0%; Score 2817; DB 9; Length 2817;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAATATATCCCTCTACCAACTGCGCATTTCAAACCGTTTCATTTCCAAACATCG 60
Db 1 AATGAATATATCCCTCTACCAACTGCGCATTTCAAACCGTTTCATTTCCAAACATCG 60
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Db 421 TGGCGCATTTCAACAGTTGACGCTGCAAAAAGCCGACCTCCGCAATGCACTAAGCCC 480
QY 481 GATTGATCTCACTAGCAATAGTCAAGTGGCCGCTGTGATGTAATTTGGCTGGAGAAATGG 540
Db 481 GATTGATCTCACTAGCAATAGTCAAGTGGCCGCTGTGATGTAATTTGGCTGGAGAAATGG 540
QY 541 CGAATATTTTCTTCTTCAAGTACGTCAACAGTGAATCCAAAGTGCAGTGGAGCGGT 600
Db 541 CGAATATTTTCTTCTTCAAGTACGTCAACAGTGAATCCAAAGTGCAGTGGAGCGGT 600
QY 601 GACCTGCGATGAGCGCTGATCTATAGCAATGAGATACAGTTGAAATACGATCACAT 660
Db 601 GACCTGCGATGAGCGCTGATCTATAGCAATGAGATACAGTTGAAATACGATCACAT 660
QY 661 CTTCACCAACATCGGTGTGAGAGAGAGATGCCGCTCAACGTTTCATGTTGGGCA 720
Db 661 CTTCACCAACATCGGTGTGAGAGAGAGATGCCGCTCAACGTTTCATGTTGGGCA 720
QY 721 GTTGGACACCACTTCTCCAAACGTGTGAGGTTGACCGTTTGAATCCGTTCCATTCAAGC 780
Db 721 GTTGGACACCACTTCTCCAAACGTGTGAGGTTGACCGTTTGAATCCGTTCCATTCAAGC 780
QY 781 TGGTGCTACCCCGCTGAGGTTGCGAGAAAATCTGGAAGAGTGGAGCAATGCGCTGC 840
Db 781 TGGTGCTACCCCGCTGAGGTTGCGAGAAAATCTGGAAGAGTGGAGCAATGCGCTGC 840
QY 841 GTCTTATGTTTCCCTGTGTCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTGTGT 900
Db 841 GTCTTATGTTTCCCTGTGTCGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTGTGT 900
QY 901 GCTGTTGGGTGAGTGGAGGTTTCCCTAATTTGCTTTATTAACGCGCTTCAACGATCAT 960
Db 901 GCTGTTGGGTGAGTGGAGGTTTCCCTAATTTGCTTTATTAACGCGCTTCAACGATCAT 960
QY 961 TGGCAGACGTCATTTTGGGAAAAGAAAGGTTTGGCTTCTTCCAAAATGTTGG 1020
Db 961 TGGCAGACGTCATTTTGGGAAAAGAAAGGTTTGGCTTCTTCCAAAATGTTGG 1020
QY 1021 TGGTTTATTTGCAACGCTGCTGCATGATGATTTGCTTATTTTGGCTTGAATTTGGTCT 1080
Db 1021 TGGTTTATTTGCAACGCTGCTGCATGATGATTTGCTTATTTTGGCTTGAATTTGGTCT 1080

QY 1081 TGAATCAAAACGAGCCAGATCATCGATCTGAAATGTTGTGCTGTTGGAGGTTTGAAC 1140
Db 1081 TGAATCAAAACGAGCCAGATCATCGATCTGAAATGTTGTGCTGTTGGAGGTTTGAAC 1140
QY 1141 ACTTGTGAATCTCTGCAGAGACGCGATACGCGGCTCTCGGTGACAGCAAGTGCAGAT 1200
Db 1141 ACTTGTGAATCTCTGCAGAGACGCGATACGCGGCTCTCGGTGACAGCAAGTGCAGAT 1200
QY 1201 TTTTGAAAACCTCCGTTTACCGCGGATTTGCTGCGGCTTGGGCTTGGGATTCACCT 1260
Db 1201 TTTTGAAAACCTCCGTTTACCGCGGATTTGCTGCGGCTTGGGCTTGGGATTCACCT 1260
QY 1261 TTTGGAATCTTGCATGATGATGTTGCTGCGATGAGTCCGCTGAGCACTAATTTATTC 1320
Db 1261 TTTGGAATCTTGCATGATGATGTTGCTGCGATGAGTCCGCTGAGCACTAATTTATTC 1320
QY 1321 GTTCAATTCGCGCCGATTTATGCTGTGTGAGCTACCGAGCGGCTTTCGAGTGGGTTG 1380
Db 1321 GTTCAATTCGCGCCGATTTATGCTGTGTGAGCTACCGAGCGGCTTTCGAGTGGGTTG 1380
QY 1381 TTAGCGGAGTGTCTTCGATGATTTAGGGGGCTTACCTGCGCTGATGAGGTTTCGCTT 1440
Db 1381 TTAGCGGAGTGTCTTCGATGATTTAGGGGGCTTACCTGCGCTGATGAGGTTTCGCTT 1440
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Db 1441 TTATTAACCTCTTCGTTGTTATTTAGGCCCGCTCTGCGCTGCGATGCTGCAACAGC 1500
QY 1501 AGTTGTTTCACTGTGTGTTGCTTGGCCGCTGATTTCTTGAATTCACCGTTGATTTGGC 1560
Db 1501 AGTTGTTTCACTGTGTGTTGCTTGGCCGCTGATTTCTTGAATTCACCGTTGATTTGGC 1560
QY 1561 GATTGCGGATCAACACCAATGCTTCAGAGCTTGAAGTTTACCGGGAATGTAAGCGAC 1620
Db 1561 GATTGCGGATCAACACCAATGCTTCAGAGCTTGAAGTTTACCGGGAATGTAAGCGAC 1620
QY 1621 CTGGAATGATCAAAACCTCATGAGTTTCACCAACATGCGGTTGCTTTAGCACCTGCTTC 1680
Db 1621 CTGGAATGATCAAAACCTCATGAGTTTCACCAACATGCGGTTGCTTTAGCACCTGCTTC 1680
QY 1681 ATCACTTGGCGCTGGGCTGTTTGGGTGATGATTTGCCGAGGCTACGTCCTCAAC 1740
Db 1681 ATCACTTGGCGCTGGGCTGTTTGGGTGATGATTTGCCGAGGCTACGTCCTCAAC 1740
QY 1741 ACGCTCAACCCATACCGTGCATTTTACCAAGGGGAATGAGTTCTCTTCAAGAGGAAGC 1800
Db 1741 ACGCTCAACCCATACCGTGCATTTTACCAAGGGGAATGAGTTCTCTTCAAGAGGAAGC 1800
QY 1801 TGAAGCAATCAGGCGCGGAGAGAAAAGCTCCAAAGACTAATCAAGATTCGGTAATA 1860
Db 1801 TGAAGCAATCAGGCGCGGAGAGAAAAGCTCCAAAGACTAATCAAGATTCGGTAATA 1860
QY 1861 AAGGTAAATTCAAACCTGCTTAGGCGCTTTCGTTAAATAGGTAGAAATTCGGGTGGA 1920
Db 1861 AAGGTAAATTCAAACCTGCTTAGGCGCTTTCGTTAAATAGGTAGAAATTCGGGTGGA 1920
QY 1921 TCGCTTTTAAACACTCAGAGAGATTCCTGCGGCAAAATCAAGCACTCGTCCACCC 1980
Db 1921 TCGCTTTTAAACACTCAGAGAGATTCCTGCGGCAAAATCAAGCACTCGTCCACCC 1980
QY 1981 CAGATATCCTTCAACGCTGTGTAAGAGAAAAGCAGCGGAGTCCGCAAGATTTGTCGA 2040
Db 1981 CAGATATCCTTCAACGCTGTGTAAGAGAAAAGCAGCGGAGTCCGCAAGATTTGTCGA 2040
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Db 2041 CCTATTCTAAGGACTTCTTCAAGGAGTCACTTTGATGTCATGCTCGGCTTGAACCTC 2100
QY 2101 AAGGCTGCGTTACACCAAGGTCCTTCTGAACACAGAGAAAGTCCCAAGAGGCTTA 2160
Db 2101 AAGGCTGCGTTACACCAAGGTCCTTCTGAACACAGAGAAAGTCCCAAGAGGCTTA 2160
QY 2161 CAAAGCGAGCTGTTAAGGACCAAGCTTAAGAGGCTGCTGCTAAGAAAAGCAAGCAAGA 2220

Db 2161 CAAAGCGACTCGTAGGCAACCACTAAGAGCGCTGCTAAGAAAAGCAAGAGGA 2220
Qy 2221 CCACCTAAGAAACTACTAAAAAGACCAACCGCAAGAAAGACCAAGAGCTTTAAGCG 2280
Db 2221 CCACCTAAGAAACTACTAAAAAGACCAACCGCAAGAAAGACCAAGAGCTTTAAGCG 2280
Qy 2281 GATCTTATATGATGATTCATTAAGCTTTGATGTTGCTAACCCTGCTGCAAGTATA 2340
Db 2281 GATCTTATATGATGATTCATTAAGCTTTGATGTTGCTAACCCTGCTGCAAGTATA 2340
Qy 2341 TGACTGTCCACCCAGATGTGTGCTATACATCTCCCCAGCCGCGTGGCTGTCAAG 2400
Db 2341 TGACTGTCCACCCAGATGTGTGCTATACATCTCCCCAGCCGCGTGGCTGTCAAG 2400
Qy 2401 GGCCTTCCCGCTTCTGGAACAACATCGTGAATGTTGGGTGCGATGAGCGCTGAAG 2460
Db 2401 GGCCTTCCCGCTTCTGGAACAACATCGTGAATGTTGGGTGCGATGAGCGCTGAAG 2460
Qy 2461 ATGTTGACCCGGAACCATTTGGAACAGATAGCGGTGTTTGTGTCACCTGTTCTCA 2520
Db 2461 ATGTTGACCCGGAACCATTTGGAACAGATAGCGGTGTTTGTGTCACCTGTTCTCA 2520
Qy 2521 CTGCAAGGACATATGAAGCTTTACAGAGGCTTTTCAAGCAACGCTGTGCTCTT 2580
Db 2521 CTGCAAGGACATATGAAGCTTTACAGAGGCTTTTCAAGCAACGCTGTGCTCTT 2580
Qy 2581 TCCACGATTTGATTTGATCTCCGCTGTATCAACACCGATTTGTGATGCTTCCGGAAG 2640
Db 2581 TCCACGATTTGATTTGATCTCCGCTGTATCAACACCGATTTGTGATGCTTCCGGAAG 2640
Qy 2641 TAAACCTCAAGTTGCTGAGACCGCTGAGCCAGAGTGGCGGCAACGCTGTGATTTGA 2700
Db 2641 TAAACCTCAAGTTGCTGAGACCGCTGAGCCAGAGTGGCGGCAACGCTGTGATTTGA 2700
Qy 2701 TGCAGGACATATGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
Db 2701 TGCAGGACATATGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
Qy 2761 AGATGGGTTCTTCTCCACATTCCTTCCCTGATCTGTTCCGTCAGCTGC 2817
Db 2761 AGATGGGTTCTTCTCCACATTCCTTCCCTGATCTGTTCCGTCAGCTGC 2817

RESULT 4
US-09-783-388-1
Sequence 1, Application US/09783388
Patent No. US20020168731A1
GENERAL INFORMATION:
APPLICANT: Ziegler, Petra
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
APPLICANT: Thierbach, Georg
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
TITLE OF INVENTION: ENZYMAIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
FILE REFERENCE: 21123/277066
CURRENT APPLICATION NUMBER: US/09/783,388
CURRENT FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 2817
TYPE: DNA
ORGANISM: Corynebacterium glutamicum ATCC14752
FEATURE:
NAME/KEY: CDS
LOCATION: (398)..(1864)
US-09-783-388-1

Query Match 100.0%; Score 2817; DB 9; Length 2817;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGAATTAATCCCTCAGCACTGGGACATTGAAAACCGTTTCATTTCCAAACATCG 60
Db 1 AATGAATTAATCCCTCAGCACTGGGACATTGAAAACCGTTTCATTTCCAAACATCG 60
Qy 61 AGCCAAAGGAAAGAAAGAGCCCTTAAGCCCGCTGTATTAATTAAGAGACTTTTGAAGCC 120
Db 61 AGCCAAAGGAAAGAAAGAGCCCTTAAGCCCGCTGTATTAATTAAGAGACTTTTGAAGCC 120
Qy 121 TCAAGCAAAAAGGGGCAATTTTCAATTAAGAAATTAACCCCTTTGACCTGCTATATGAGC 180
Db 121 TCAAGCAAAAAGGGGCAATTTTCAATTAAGAAATTAACCCCTTTGACCTGCTATATGAGC 180
Qy 181 TGGAGAAAGAGCTGAAGCTTCAACCTAAGCATTAAGAGTGGCTGCTGCTCAATTTGCG 240
Db 181 TGGAGAAAGAGCTGAAGCTTCAACCTAAGCATTAAGAGTGGCTGCTGCTCAATTTGCG 240
Qy 241 CCACCTCAGCACCGCAGATGCTGATGATCAACCACTACGAATACGATCTTAGCGTATGT 300
Db 241 CCACCTCAGCACCGCAGATGCTGATGATCAACCACTACGAATACGATCTTAGCGTATGT 300
Qy 301 GTACATCAATTGAATTTGGGGCTAAGATCTGTGTGTAACCGTCAATTAAGACCTGTG 360
Db 301 GTACATCAATTGAATTTGGGGCTAAGATCTGTGTGTAACCGTCAATTAAGACCTGTG 360
Qy 361 AATGGACTCTTTTCTCTGCAAAATGTTTCCAGCGAGATGTTGAGTTTGGGACCTTGC 420
Db 361 AATGGACTCTTTTCTCTGCAAAATGTTTCCAGCGAGATGTTGAGTTTGGGACCTTGC 420
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Db 481 GATTATCTCTACTGACCAATGATCAAGTGGCGGTGTGATTAATTTGGTGGCAAGATTTG 540
Qy 541 CGATATTTTGGCTTTCTTCAAGTACGCTCAAAAGATGATCAAGTGTGCAAGTTGCAAGCT 600
Db 541 CGATATTTTGGCTTTCTTCAAGTACGCTCAAAAGATGATCAAGTGTGCAAGTTGCAAGCT 600
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Db 601 GACCTCTGATATGAGCTGATCAATGATGATGATGATGATGATGATGATGATGATGAT 660
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Db 721 GTTGAACACCACTTCTCAAACTGTCTGAGGTTGACCGTTGATCGTTCAATTCAGGC 780
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Db 781 TGGTGTACCCCGCTGAGCTTGGCGAAGAAATTTGACAGAGTGGAGCAATCGCTGC 840
Qy 841 GTCTTATGTTTCCCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 GTCTTATGTTTCCCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Qy 901 GCTGTTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 901 GCTGTTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 961 TGCACAGCTGATTTTGGGAAAGAGGTTTGGCTACTTCTTCCAAATATGTTGTTG 1020
Db 961 TGCACAGCTGATTTTGGGAAAGAGGTTTGGCTACTTCTTCCAAATATGTTGTTG 1020
Qy 1021 TGGTTTATTTGACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 TGGTTTATTTGACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1080

1081 TGAGATCAACCGAGCCAGATCATGCAATGGAAATGGTGGCTGGTGGCAGGTTTGAC 1140
1081 TGAGATCAACCGAGCCAGATCATGCAATGGAAATGGTGGCTGGTGGCAGGTTTGAC 1140
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1141 ACTGTGCAATCTCTGCAAGACCGGATCAAGGCGCTCCGGTGAAGAGAGGACGAT 1200
1201 TTTTGAACACTCTCTGTTTACCGGCGGCAATGTGTGGCGGTGGGTTTGGCAATTCAGCT 1260
1201 TTTTGAACACTCTCTGTTTACCGGCGGCAATGTGTGGCGGTGGGTTTGGCAATTCAGCT 1260
1261 TTCTGAATCTGTGATGTCATGTTGCTGGCAATGAGATGCTGCTGACAGACTTAATATTC 1320
1261 TTCTGAATCTGTGATGTCATGTTGCTGGCAATGAGATGCTGCTGACAGACTTAATATTC 1320
1321 GTCTACATTCGCGCGCATTAATGCTGTGTGCGTCAACGAGCGGCGCTTGGCAGTGGGTTG 1380
1321 GTCTACATTCGCGCGCATTAATGCTGTGTGCGTCAACGAGCGGCGCTTGGCAGTGGGTTG 1380
1381 TTACGCGGAGTGTCTCTGCGTGAATTTGCGGGGCTTACTGCGCTGATGGGTTTCTGGCTT 1440
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1501 AGTTGGTTTCACTGTTGTTGCTTGGCGCTGCAATCTTGAATTCACGTTGAATGGG 1560
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1561 GATTGCGCGGATCAACCAATGCTTCCAGGCTTACGCAATTTACCGCGAAATGTAAGCGCAC 1620
1621 CTGAATGATCAACACTCACTGAGGTTTCAACAATTTGCGGCTGCTTACCGACTGCTTC 1680
1621 CTGAATGATCAACACTCACTGAGGTTTCAACAATTTGCGGCTGCTTACCGACTGCTTC 1680
1681 ATCACTTCCGCGTGGCGGTGTTTGGGTGATGAGATTCGCGGAGGCTACGCTGCTCACCC 1740
1681 ATCACTTCCGCGTGGCGGTGTTTGGGTGATGAGATTCGCGGAGGCTACGCTGCTCACCC 1740
1741 AGCTTCAACCCATACCTGTCATTTACCAAGGCGAAATGAGTTCCTTCCAGAGAGAAAG 1800
1741 AGCTTCAACCCATACCTGTCATTTACCAAGGCGAAATGAGTTCCTTCCAGAGAGAAAG 1800
1801 TGAGCAGATCAAGCGCGGAGAGAAAGTCCAAAGACTAATCAAAAGATTCGTAATTA 1860
1801 TGAGCAGATCAAGCGCGGAGAGAAAGTCCAAAGACTAATCAAAAGATTCGTAATTA 1860
1861 AAGGTAATAATCAACCTGCTTAGGCGCTTTCGTTAAATAGCGTAATTCGAGGTGCA 1920
1861 AAGGTAATAATCAACCTGCTTAGGCGCTTTCGTTAAATAGCGTAATTCGAGGTGCA 1920
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1921 TGGCTTTTAAACTCAGAGAGATCTTCCCGGCGCAAAATCAAGCACTGCTCCACCC 1980
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1921 TGGCTTTTAAACTCAGAGAGATCTTCCCGGCGCAAAATCAAGCACTGCTCCACCC 1980
1981 CAGAAATCCCTTCAAGCTGTTGAAGAGAAACCGAGCGGCTCCGCGAGAGATTTGGTCCA 2040
1981 CAGAAATCCCTTCAAGCTGTTGAAGAGAAACCGAGCGGCTCCGCGAGAGATTTGGTCCA 2040
1981 CAGAAATCCCTTCAAGCTGTTGAAGAGAAACCGAGCGGCTCCGCGAGAGATTTGGTCCA 2040
2041 CCTATTCTAAGGACTTCTTCAAGCGGCTCACTTTGATGTCATGCTCGGCGTTGAACCTC 2100
2041 CCTATTCTAAGGACTTCTTCAAGCGGCTCACTTTGATGTCATGCTCGGCGTTGAACCTC 2100
2101 AGGGCTCGGTATCAACCAAGGCTGCTTGAACAGAGAAAGCTCAAGCCAAAGAGAGCTTA 2160
2101 AGGGCTCGGTATCAACCAAGGCTGCTTGAACAGAGAAAGCTCAAGCCAAAGAGAGCTTA 2160
2101 AGGGCTCGGTATCAACCAAGGCTGCTTGAACAGAGAAAGCTCAAGCCAAAGAGAGCTTA 2160
2161 CAAAGCGGACTCGTAAGGCAACAGCTAAGAAAGGCTGCTGTAAGAAAGAGCAACCAAGAGA 2220

2161 CAAAGCGGACTCGTAAGGCAACAGCTAAGAAAGGCTGCTGCTAAGAAAGAGCAACCAAGAGA 2220
2221 CCCTAAGAAAGACTACTAAGAAAGCAACCGCAAGAAAGAGCAACCAAGAGCTTAAAGCG 2280
2221 CCCTAAGAAAGACTACTAAGAAAGCAACCGCAAGAAAGAGCAACCAAGAGCTTAAAGCG 2280
2281 GATCTTATATGATGATTTCCAAATGCTTGTGATGTTGTTGCTAATCCGTGTGCAATGATA 2340
2281 GATCTTATATGATGATTTCCAAATGCTTGTGATGTTGTTGCTAATCCGTGTGCAATGATA 2340
2341 TGACTGTCAACCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
2341 TGACTGTCAACCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
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2401 GGGCTTCCCGCTTCTGGAACCAATGCTGATGATGATGATGATGATGATGATGATGATGAT 2460
2401 GGGCTTCCCGCTTCTGGAACCAATGCTGATGATGATGATGATGATGATGATGATGATGAT 2460
2461 ATGTTGCAACCGGAAACATTTGGAACAGATGATGATGATGATGATGATGATGATGATGATGAT 2520
2461 ATGTTGCAACCGGAAACATTTGGAACAGATGATGATGATGATGATGATGATGATGATGATGAT 2520
2521 CTGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
2521 CTGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
2581 TCCACGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
2581 TCCACGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
2641 TAAACCTCAAGTTCGCTGAAGCGGTGAGCGCAAGTGGGCGGCAACGCGGCACTGTGGG 2700
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2701 TGCAGGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
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2761 AGATGCGTTTCTTCCCAATTCCTCCCTTCCCTGATGCTGTTCCGTAAGCTGC 2817
2761 AGATGCGTTTCTTCCCAATTCCTCCCTTCCCTGATGCTGTTCCGTAAGCTGC 2817

RESULT 5
US-09-951-535-1
; Sequence 1, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMIC PRODUCTION OF L-THREONINE
; FILE REFERENCE: 21123/28245/MAS
; CURRENT APPLICATION NUMBER: US/09/951, 535
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431, 099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478-5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: tnf-Gen

US-09-951-535-1

Query Match	100.0%	Score 2817	DB 10	Length 2817
Best Local Similarity	100.0%	Pred No. 0		
Matches 2817	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	AATGAATATATCCCTCACCACCTGGGACATTCAAACACCGTTTCATTTCCAAACATCG	60	
DB	1	AATGAATATATCCCTCACCACCTGGGACATTCAAACACCGTTTCATTTCCAAACATCG	60	
QY	61	AGCCAAAGGAAAAAGAAAGCCCTTAAGCCCGCTGTATTAATGAGAGCTCTGGAGACC	120	
DB	61	AGCCAAAGGAAAAAGAAAGCCCTTAAGCCCGCTGTATTAATGAGAGCTCTGGAGACC	120	
QY	121	TCAAGCCAAAAAGGGGATTTTCAATTAAGAAATATCCCTTTGACCTGTGTATTGAGC	180	
DB	121	TCAAGCCAAAAAGGGGATTTTCAATTAAGAAATATCCCTTTGACCTGTGTATTGAGC	180	
QY	181	TGAGAAAGAGACTTGAACCTGCAACCTAAGCATTAACAAGTCGCTGGCTGCCAATTGGC	240	
DB	181	TGAGAAAGAGACTTGAACCTGCAACCTAAGCATTAACAAGTCGCTGGCTGCCAATTGGC	240	
QY	241	CCACTCCAGCACCCGAGATGCTGATGATCAACAATACGATACGTAATCTTAGCGTATGT	300	
DB	241	CCACTCCAGCACCCGAGATGCTGATGATCAACAATACGATACGTAATCTTAGCGTATGT	300	
QY	301	GTAATCAACAATGSAATTCGGGGCTAGAGATCTGTGAGAACCGTGCAATMAACGACTGTG	360	
DB	301	GTAATCAACAATGSAATTCGGGGCTAGAGATCTGTGAGAACCGTGCAATMAACGACTGTG	360	
QY	361	ATTGGAATCTTTTCTTTCTTGCAAAATGTTTTCCAGGAGATGTGATTTGGAGACCTTGG	420	
DB	361	ATTGGAATCTTTTCTTTCTTGCAAAATGTTTTCCAGGAGATGTGATTTGGAGACCTTGG	420	
QY	421	TGCGCCGATTTTCAACAGTTGAGCGGTGCAAAAGCCGCACTCCGCGCATGCGCAATGCCC	480	
DB	421	TGCGCCGATTTTCAACAGTTGAGCGGTGCAAAAGCCGCACTCCGCGCATGCGCAATGCCC	480	
QY	481	GATTGATCTCACTGACATAGTCAAGTGGCGGTGTGATGAAATTTGCTGCGAGAAATGG	540	
DB	481	GATTGATCTCACTGACATAGTCAAGTGGCGGTGTGATGAAATTTGCTGCGAGAAATGG	540	
QY	541	CGATATTTTGTCTTCTTCAAGTACGTCAACAGTATACCAAGGTGCAAGTTCCAGCGGT	600	
DB	541	CGATATTTTGTCTTCTTCAAGTACGTCAACAGTATACCAAGGTGCAAGTTCCAGCGGT	600	
QY	601	GACCTTCGCGATGSCCTGATCTATAGCATGTGATATCAAGTTGAATACGATACCAT	660	
DB	601	GACCTTCGCGATGSCCTGATCTATAGCATGTGATATCAAGTTGAATACGATACCAT	660	
QY	661	CTTCAACCAACATCGGTGTGAGAGAGAAATGCGGTCAACGTTTCATGTTGTGGGCA	720	
DB	661	CTTCAACCAACATCGGTGTGAGAGAGAAATGCGGTCAACGTTTCATGTTGTGGGCA	720	
QY	721	GTTGAGACCAACTTCTTCAAACTGTCTGAGTTGACCGTTGATCCGTTCCATTCAAGC	780	
DB	721	GTTGAGACCAACTTCTTCAAACTGTCTGAGTTGACCGTTGATCCGTTCCATTCAAGC	780	
QY	781	TGATGTACCCCGCGCTGAGAGTTGCCGAGAAATTTGAGAGAGTTGAGCAATTCGCTGC	840	
DB	781	TGATGTACCCCGCGCTGAGAGTTGCCGAGAAATTTGAGAGAGTTGAGCAATTCGCTGC	840	
QY	841	GTTCTTAATGCTTCCCTGTTGCTGCTTGGCTGGGCAATGATGGGTGGCTGTGCTGT	900	
DB	841	GTTCTTAATGCTTCCCTGTTGCTGCTTGGCTGGGCAATGATGGGTGGCTGTGCTGT	900	
QY	901	GCTGTGTTGGGTGTGATGAGAGTTTCCCTAATGCTTTTATTAACCGCGTTCAAGATCAT	960	
DB	901	GCTGTGTTGGGTGTGATGAGAGTTTCCCTAATGCTTTTATTAACCGCGTTCAAGATCAT	960	
QY	961	TGCGACGAGCTATTTTGGGAAAAAGAGGTTTGCCTACTTTTCCAAATGTTGTGG	1020	
DB	961	TGCGACGAGCTATTTTGGGAAAAAGAGGTTTGCCTACTTTTCCAAATGTTGTGG	1020	

QY	1021	TGGTTTTTATGCGAGGCTGCTGCATGATGCTTATTTCTTTGGCGTTGCAATTTGAGTCT	1080	
DB	1021	TGGTTTTTATGCGAGGCTGCTGCATGATGCTTATTTCTTTGGCGTTGCAATTTGAGTCT	1080	
QY	1081	TGAGATCAAAACCGAGCGAGATCATGCAATCTGGAAATGTTGTGTGTGTGGCAGGTTTAC	1140	
DB	1081	TGAGATCAAAACCGAGCGAGATCATGCAATCTGGAAATGTTGTGTGTGTGGCAGGTTTAC	1140	
QY	1141	ACTTGTGCAATCTCTGAGAGAGCGCATCACGGGCGCTCCGGGTGACAGCAATGCAAGAT	1200	
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QY	1201	TTTTGAAAGCATCTGCTTTTACCGGCGGATTTGTTGCTGCGGTGGGTTTGGGCAATTCAGCT	1260	
DB	1201	TTTTGAAAGCATCTGCTTTTACCGGCGGATTTGTTGCTGCGGTGGGTTTGGGCAATTCAGCT	1260	
QY	1261	TTCTGAAATCTGCAATGTCATGTTGCTGCTGCAATGAGTCCGCTGACACCTTAATTTTC	1320	
DB	1261	TTCTGAAATCTGCAATGTCATGTTGCTGCTGCAATGAGTCCGCTGACACCTTAATTTTC	1320	
QY	1321	GTTTACATTTGCGCGCATTTATGCTGTGGGTGCTACCGAGCGGCTTTCAGTGGGTTG	1380	
DB	1321	GTTTACATTTGCGCGCATTTATGCTGTGGGTGCTACCGAGCGGCTTTCAGTGGGTTG	1380	
QY	1381	TTACGCGAGAGTGTCTCGGATTTATGCGGGCTTACTGCGCTGATGAGGTTTGTGCTT	1440	
DB	1381	TTACGCGAGAGTGTCTCGGATTTATGCGGGCTTACTGCGCTGATGAGGTTTGTGCTT	1440	
QY	1441	TTATTAACCTCTGCTGTTTATTTAAGCCCGCTCTGCGCGCTGCAATGCTGCAACAGC	1500	
DB	1441	TTATTAACCTCTGCTGTTTATTTAAGCCCGCTCTGCGCGCTGCAATGCTGCAACAGC	1500	
QY	1501	AGTTGTTTCACTGTGTGTTTGTGCTGCGCGCTGCAATGCTGCAACAGTGTGTTGGC	1560	
DB	1501	AGTTGTTTCACTGTGTGTTTGTGCTGCGCGCTGCAATGCTGCAACAGTGTGTTGGC	1560	
QY	1561	GATTGCGGCAATCAACCAATGCTTCAAGTCTAGCAATTTACCGGAGATGTAAGCCAC	1620	
DB	1561	GATTGCGGCAATCAACCAATGCTTCAAGTCTAGCAATTTACCGGAGATGTAAGCCAC	1620	
QY	1621	CTTGAATGATCAAAACATCATGAGTTTTCACCAATTCGCGGTGTTTAGCACTGCTTC	1680	
DB	1621	CTTGAATGATCAAAACATCATGAGTTTTCACCAATTCGCGGTGTTTAGCACTGCTTC	1680	
QY	1681	ATCACTTCCGCTGCGGTGTTTGGGTGAGTGAATGCGGCAAGCTACGTCGTCACC	1740	
DB	1681	ATCACTTCCGCTGCGGTGTTTGGGTGAGTGAATGCGGCAAGCTACGTCGTCACC	1740	
QY	1741	ACGCTTCAACCATCAACGCTGCAATTTACCAAGGCGAATGATTCTCTTCCAGAGAGAAC	1800	
DB	1741	ACGCTTCAACCATCAACGCTGCAATTTACCAAGGCGAATGATTCTCTTCCAGAGAGAAC	1800	
QY	1801	TGAGCAAGTACAGCGCGCGAGAGAAAGTCCAAAGCTAATCAAAAGTTGGTAAATTA	1860	
DB	1801	TGAGCAAGTACAGCGCGCGAGAGAAAGTCCAAAGCTAATCAAAAGTTGGTAAATTA	1860	
QY	1861	AAGGTAAATATCAACCTGCTTGGCGTCTTTCGTTAAATAGCGAATATCGGCTGCA	1920	
DB	1861	AAGGTAAATATCAACCTGCTTGGCGTCTTTCGTTAAATAGCGAATATCGGCTGCA	1920	
QY	1921	TGCTTTTAAACATCAGAGAGATCTTTCGCGGCAAAATACAGCAACTCGTCCACCC	1980	
DB	1921	TGCTTTTAAACATCAGAGAGATCTTTCGCGGCAAAATACAGCAACTCGTCCACCC	1980	
QY	1981	CAGATCCCTTCAACGCTGTGTAAGAGAAACGAGCGGCTGCCGAGATTTGTTGCCA	2040	
DB	1981	CAGATCCCTTCAACGCTGTGTAAGAGAAACGAGCGGCTGCCGAGATTTGTTGCCA	2040	
QY	2041	CCATATCTAAGGACTTCTTCAACGCGGTCACTTGTGATGTCATGCTCGGCTTGAACCTTC	2100	
DB	2041	CCATATCTAAGGACTTCTTCAACGCGGTCACTTGTGATGTCATGCTCGGCTTGAACCTTC	2100	

QY 2101 AGGCGCTCGTTACACCAAGGTCGCTTCTGAAACAGAGAGAGCTCAGCCAAAGAGCTA 2160
DB 2101 AGGCGCTCGTTACACCAAGGTCGCTTCTGAAACAGAGAGAGCTCAGCCAAAGAGCTA 2160
QY 2161 CAAACCGGACTCGTAAAGGACCCAGCTAAAGAGAGCTGCTTAAGAAAAGACCAAGAGA 2220
DB 2161 CAAACCGGACTCGTAAAGGACCCAGCTAAAGAGAGCTGCTTAAGAAAAGACCAAGAGA 2220
QY 2221 CCACCTAAAGAAACTCACTAAAAAGACCAACCGCAAGAGAACCAAAAGAGCTTAAAGCG 2280
DB 2221 CCACCTAAAGAAACTCACTAAAAAGACCAACCGCAAGAGAACCAAAAGAGCTTAAAGCG 2280
QY 2281 GATCTTATAGATGATTCGAAATGAGCTTTGATGTTGCTTAACCGTTCGCAAGTATA 2340
DB 2281 GATCTTATAGATGATTCGAAATGAGCTTTGATGTTGCTTAACCGTTCGCAAGTATA 2340
QY 2341 TGACTGTCCACCCAGATGATGCTAATAGCATCTCCCGACCGGTCGCTGTCACGG 2400
DB 2341 TGACTGTCCACCCAGATGATGCTAATAGCATCTCCCGACCGGTCGCTGTCACGG 2400
QY 2401 GGCCTTCCCGCTTCTGGAACAATCGTGATGTGGTGGAATGGCTTGAACCTGTAG 2460
DB 2401 GGCCTTCCCGCTTCTGGAACAATCGTGATGTGGTGGAATGGCTTGAACCTGTAG 2460
QY 2461 ATGTTCACCCGGAACCAATTCGAACAGATACGGGTGTTGCTGCAACCTGTCTCA 2520
DB 2461 ATGTTCACCCGGAACCAATTCGAACAGATACGGGTGTTGCTGCAACCTGTCTCA 2520
QY 2521 CTGCACTGACTATGAAAGGCTTCAAGAGGCTTTTAAACGCAAGCTGTGGCTCTTT 2580
DB 2521 CTGCACTGACTATGAAAGGCTTCAAGAGGCTTTTAAACGCAAGCTGTGGCTCTTT 2580
QY 2581 TCCACGATTTGATTTGATCTCCGCTGTAACAACCGATGGTGCATGCTTTTCGAGAG 2640
DB 2581 TCCACGATTTGATTTGATCTCCGCTGTAACAACCGATGGTGCATGCTTTTCGAGAG 2640
QY 2641 TAAACCTCAAGTTCGCGAGAGCGGTGAGCCAAAGTGGGCGACACGGTGCCATGTGGG 2700
DB 2641 TAAACCTCAAGTTCGCGAGAGCGGTGAGCCAAAGTGGGCGACACGGTGCCATGTGGG 2700
QY 2701 TGCAGACTATTCAGCTGTGCTGCTGCTGCAATTTTGCGCCAGATGCGCCCTGATTGA 2760
DB 2701 TGCAGACTATTCAGCTGTGCTGCTGCTGCAATTTTGCGCCAGATGCGCCCTGATTGA 2760
QY 2761 AGATCGGTTCTTCTCCACATTCCTTCCCTTCCCTGATCTGTTCCGCACTGG 2817
DB 2761 AGATCGGTTCTTCTCCACATTCCTTCCCTTCCCTGATCTGTTCCGCACTGG 2817

RESULT 6

US-10-224-574-9
; Sequence 9, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
; APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
; APPLICANT: P. Peters- Werdisch
; TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the syn
; TITLE OF INVENTION: L-Serin, improved process for the microbial manufacture of L-ser
; FILE REFERENCE: FZJ-9912-PCT
; CURRENT APPLICATION NUMBER: US/10/224,574
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: C. glutamicum ATCC 14 752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1867)
; OTHER INFORMATION: thr E (threonin-exportcarrier)
US-10-224-574-9

Query Match 100.0%; Score 2817; DB 17; Length 2817;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAATATATCCCTCCACCACTGGGACATTTAAACACCGTTTCAATTTCCAAACATCG 60
DB 1 AATGAATATATCCCTCCACCACTGGGACATTTAAACACCGTTTCAATTTCCAAACATCG 60
QY 61 AGCCAGGAAAAAGAAAGCCCTTAAAGCCCGTGTATTAATGAGACTCTTTTGAGAGCC 120
DB 61 AGCCAGGAAAAAGAAAGCCCTTAAAGCCCGTGTATTAATGAGACTCTTTTGAGAGCC 120
QY 121 TCAAGCCAAAAAGGGGCAATTTTCAATTAAGAAATATACCCCTTTGACTGTGTATGAGC 180
DB 121 TCAAGCCAAAAAGGGGCAATTTTCAATTAAGAAATATACCCCTTTGACTGTGTATGAGC 180
QY 181 TGAAGAGAGACTTGAATCTCAACTAGCATTAACAAGTGCCTTGGCGTCCAAATGGG 240
DB 181 TGAAGAGAGACTTGAATCTCAACTAGCATTAACAAGTGCCTTGGCGTCCAAATGGG 240
QY 241 CCACTCCAGCACCGCAATGCTGATGATCAACAACTAAGATATCTTAAAGCGTATGT 300
DB 241 CCACTCCAGCACCGCAATGCTGATGATCAACAACTAAGATATCTTAAAGCGTATGT 300
QY 301 GTACATCAATGGAATTTGGGGGTAGAGATCTGATGGAACCGTGCATTAACACCTGTG 360
DB 301 GTACATCAATGGAATTTGGGGGTAGAGATCTGATGGAACCGTGCATTAACACCTGTG 360
QY 361 ATGGACTCTTTTCCCTTCCGAAATGTTTCCAGCGGATGTTGATGTTTGGACCTTGG 420
DB 361 ATGGACTCTTTTCCCTTCCGAAATGTTTCCAGCGGATGTTGATGTTTGGACCTTGG 420
QY 421 TGGCCGATTTCAACAGTTGACGCTGCAAAAGCCGCACTCCGCAATGCGCACTAGCCC 480
DB 421 TGGCCGATTTCAACAGTTGACGCTGCAAAAGCCGCACTCCGCAATGCGCACTAGCCC 480
QY 481 GATTGATCAGTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 481 GATTGATCAGTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 541 CGATATTTTGTCTTCTTCAAGATACGTCAAAACAGTGAATCCAAAGTGCATGAGCGGT 600
DB 541 CGATATTTTGTCTTCTTCAAGATACGTCAAAACAGTGAATCCAAAGTGCATGAGCGGT 600
QY 601 GACCTCTGGATGATGCTGATCTAATACGATGATGATGATGATGATGATGATGATGAT 660
DB 601 GACCTCTGGATGATGCTGATCTAATACGATGATGATGATGATGATGATGATGATGAT 660
QY 661 CTTTACCAACATGCGGTGAGAGAGAGATGCGGTCACATGCTTTTCAATGTTGGGCA 720
DB 661 CTTTACCAACATGCGGTGAGAGAGAGATGCGGTCACATGCTTTTCAATGTTGGGCA 720
QY 721 GTTGAACACCAATCTTCCAACTGTCTGAGGTGACCGTTGATCGTTCCATCAGGC 780
DB 721 GTTGAACACCAATCTTCCAACTGTCTGAGGTGACCGTTGATCGTTCCATCAGGC 780
QY 781 TGGTGATCCCGGCTGAGGTGCGGAGAAATTTCTGACAGTGTGAGCAATGCGCTGG 840
DB 781 TGGTGATCCCGGCTGAGGTGCGGAGAAATTTCTGACAGTGTGAGCAATGCGCTGG 840
QY 841 GTCTATGATTTCCCGTGTGCGTGTGCGTGGCAATGATGATGATGATGATGATGATG 900
DB 841 GTCTATGATTTCCCGTGTGCGTGTGCGTGGCAATGATGATGATGATGATGATGATG 900
QY 901 GCTGTGTGGTGTGATGAGAGATTTCCCTAATGCTTTTATTAACGCGTTACAGATCAT 960
DB 901 GCTGTGTGGTGTGATGAGAGATTTCCCTAATGCTTTTATTAACGCGTTACAGATCAT 960
QY 961 TGGCAAGAGCTGATTTTGGGAAAAAGAGGTTTGCTTCTTCCAAATGTTGTTGG 1020
DB 961 TGGCAAGAGCTGATTTTGGGAAAAAGAGGTTTGCTTCTTCCAAATGTTGTTGG 1020

QY 1021 TGGTTTATTCGACGCTGCTGCATGATTCCTTATTCCTTGGCGTTGCAATTTGCTC 1080
DB 1021 TGGTTTATTCGACGCTGCTGCATGATTCCTTATTCCTTGGCGTTGCAATTTGCTC 1080
QY 1081 TGGATTCACAAACGAGCGAGATCAGCATCTGGAATGTGTGCTGTGTGCAAGTTTAC 1140
DB 1081 TGGATTCACAAACGAGCGAGATCAGCATCTGGAATGTGTGCTGTGTGCAAGTTTAC 1140
QY 1141 ACTTGTGCAATCTCTGAGAGACGCGCATCACGGGCGCTCCGCTGACACAGATGACAT 1200
DB 1141 ACTTGTGCAATCTCTGAGAGACGCGCATCACGGGCGCTCCGCTGACACAGATGACAT 1200
QY 1201 TTTTGAACACTCTGTTTACCGGCGGATTTGTCTGGGGTGGGTTTGGGCAATTCAGCT 1260
DB 1201 TTTTGAACACTCTGTTTACCGGCGGATTTGTCTGGGGTGGGTTTGGGCAATTCAGCT 1260
QY 1261 TTTGGAATCTTGAGATGATGATGCTGCGCATGAGTCCGCTGACACACTAATTTATTC 1320
DB 1261 TTTGGAATCTTGAGATGATGATGCTGCGCATGAGTCCGCTGACACACTAATTTATTC 1320
QY 1321 GTCTACATTCGCGCGCATTTATCGTGTGCGCTACCGGAGCGCTTTCGATGGGTTG 1380
DB 1321 GTCTACATTCGCGCGCATTTATCGTGTGCGCTACCGGAGCGCTTTCGATGGGTTG 1380
QY 1381 TTTACGCGAGTGTCTCGTGTGATTTATTCGCGGGCTTACTGCGTGAATGGGTTGCGGT 1440
DB 1381 TTTACGCGAGTGTCTCGTGTGATTTATTCGCGGGCTTACTGCGTGAATGGGTTGCGGT 1440
QY 1441 TTTATTAACCTCTGCTGTTTATTTAGGCGCGCTCTGCGCTGCGATGCTGCAACAGC 1500
DB 1441 TTTATTAACCTCTGCTGTTTATTTAGGCGCGCTCTGCGCTGCGATGCTGCAACAGC 1500
QY 1501 AGTTGGTTTCACTGCTGTGCTTTCCTTGCCTGATCTTGAATTCACCGTTGATTTGCGC 1560
DB 1501 AGTTGGTTTCACTGCTGTGCTTTCCTTGCCTGATCTTGAATTCACCGTTGATTTGCGC 1560
QY 1561 GATTGCGCGCATCACACCAATGCTTCAGGTCTACAAATTTACCGGGAATGTAAGCCAC 1620
DB 1561 GATTGCGCGCATCACACCAATGCTTCAGGTCTACAAATTTACCGGGAATGTAAGCCAC 1620
QY 1621 CTGGAATGATCAAACTCATGGGTTTTCACCAATTCGCTGCTTAAAGCCATGCTTC 1680
DB 1621 CTGGAATGATCAAACTCATGGGTTTTCACCAATTCGCTGCTTAAAGCCATGCTTC 1680
QY 1681 ATCACTTCCGCTGCGCTGTGTTTGGGTGATGATTCGCGGACGATACGTCGCAAC 1740
DB 1681 ATCACTTCCGCTGCGCTGTGTTTGGGTGATGATTCGCGGACGATACGTCGCAAC 1740
QY 1741 ACGTTTCAACCATACCGTGCATTTACCAAGCGGATGATTCCTTTCAGAGAGAGC 1800
DB 1741 ACGTTTCAACCATACCGTGCATTTACCAAGCGGATGATTCCTTTCAGAGAGAGC 1800
QY 1801 TGAAGCAATTCAGCGCGCGCAGAGAAAGTCCAAAGATTAACAAAGATTGCTAATA 1860
DB 1801 TGAAGCAATTCAGCGCGCGCAGAGAAAGTCCAAAGATTAACAAAGATTGCTAATA 1860
QY 1861 AAGGTAAATATCAACTGCTTAAAGGCTCTTTCGCTTAAATAGCGTAAATTCGGTCA 1920
DB 1861 AAGGTAAATATCAACTGCTTAAAGGCTCTTTCGCTTAAATAGCGTAAATTCGGTCA 1920
QY 1921 TGGCTTTTAAACACTGAGAGATCTTTCGCGGCAAAATTCAGGACATCTGCTCCACC 1980
DB 1921 TGGCTTTTAAACACTGAGAGATCTTTCGCGGCAAAATTCAGGACATCTGCTCCACC 1980
QY 1981 CAGAAATCCCTTCAGCTGTGTAAGAGAAACGACCGGCTGCGCAGATTTGTTCCA 2040
DB 1981 CAGAAATCCCTTCAGCTGTGTAAGAGAAACGACCGGCTGCGCAGATTTGTTCCA 2040
QY 2041 CCTATTCTAAGAGCTTCTTCGACGCGGTCACTTTGATGTGCATGCTCGGGGTGAACCTC 2100
DB 2041 CCTATTCTAAGAGCTTCTTCGACGCGGTCACTTTGATGTGCATGCTCGGGGTGAACCTC 2100
QY 2101 AAGGCTGCGTTACCAAGGTGCTTTCGACACGAGAGAGCTGACCAAGAGGCTA 2160

DB 2101 AAGGCTGCGTTACCAAGGTGCTTTCGACACGAGAGAGCTGACCAAGAGGCTA 2160
QY 2161 CAAGCGGACTCTTAAAGGACCAAGCTTAAAGAGGCTGTGCTAAAGAAACGACCAAGAGA 2220
DB 2161 CAAGCGGACTCTTAAAGGACCAAGCTTAAAGAGGCTGTGCTAAAGAAACGACCAAGAGA 2220
QY 2221 CCACTAAGAAACTTAAAGAAACGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
DB 2221 CCACTAAGAAACTTAAAGAAACGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
QY 2281 GATCTTATATGATGATTCCTTAAAGCTTGTGATTTGCTTAAACCTGCTCCGATGATA 2340
DB 2281 GATCTTATATGATGATTCCTTAAAGCTTGTGATTTGCTTAAACCTGCTCCGATGATA 2340
QY 2341 TGACTGTCCACCAAGATGATGATTAAGCATTCCTCCAGCGCGGCGGCTGCTGACGG 2400
DB 2341 TGACTGTCCACCAAGATGATGATTAAGCATTCCTCCAGCGCGGCGGCTGCTGACGG 2400
QY 2401 GGGTTTCCCGGTTCTGGAACCAACATGCTGATGTTGGGTGATGCTGGAACCTGTAG 2460
DB 2401 GGGTTTCCCGGTTCTGGAACCAACATGCTGATGTTGGGTGATGCTGGAACCTGTAG 2460
QY 2461 ATGTTGACCCGAAACATTTGAAACAGATACGGGTTTGTCTGCAACCTGCTGCTCA 2520
DB 2461 ATGTTGACCCGAAACATTTGAAACAGATACGGGTTTGTCTGCAACCTGCTGCTCA 2520
QY 2521 CTGCAAGTACTAAGAGGCTTCTACAGAGGCTTTCAAAGCAACGCTGTGCTCTTT 2580
DB 2521 CTGCAAGTACTAAGAGGCTTCTACAGAGGCTTTCAAAGCAACGCTGTGCTCTTT 2580
QY 2581 TCCAGATTTGATTTACTCTCGGTGTACCAACCGATTTGCTGCTGCTTGGGAG 2640
DB 2581 TCCAGATTTGATTTACTCTCGGTGTACCAACCGATTTGCTGCTGCTTGGGAG 2640
QY 2641 TAAACTCAAGTTGCTTGAACCGGTGAGCCAAAGTGGCGGCAACGCTGCACTGTGAG 2700
DB 2641 TAAACTCAAGTTGCTTGAACCGGTGAGCCAAAGTGGCGGCAACGCTGCACTGTGAG 2700
QY 2701 TGCAGGACTATAGAGCTGTTGCTGATTCCTGCAATTTTGGCAGATTTGGCCAGATTTGA 2760
DB 2701 TGCAGGACTATAGAGCTGTTGCTGATTCCTGCAATTTTGGCAGATTTGGCCAGATTTGA 2760
QY 2761 AGATGCTTCTCTCTCCACATTCCTTCCCTTCCCTGATCTGTCGTGAGCTGC 2817
DB 2761 AGATGCTTCTCTCTCCACATTCCTTCCCTTCCCTGATCTGTCGTGAGCTGC 2817

RESULT 7
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIRO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SRO ID NO: 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
us-09-738-626-1

Query Match 98.8%; Score 2783.4; DB 9; Length 3309400;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2796; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 AATGAATTAATCCCTCAACCACTGGGACATTCAACACCGCTTTCATTCCAAACATCG 60
Db 2790585 AATGAATTAATCCCTCAACCACTGGGACATTCAACACCGCTTTCATTCCAAACATCG 2790644
QY 61 AGCCAGGAGAAAGAAAGCCCTTAAGCCCGTGTATTAAATGAGAGACTCTTGGAGACC 120
Db 2790645 AGCCAGGAGAAAGAAAGCCCTTAAGCCCGTGTATTAAATGAGAGACTCTTGGAGACC 2790704
QY 121 TCAGGCCAAAAGGGGCAATTTTCATTAGAAAATATACCCCTTTGAACCTGCTTATTGAGC 180
Db 2790705 TCAGGCCAAAAGGGGCAATTTTCATTAGAAAATATACCCCTTTGAACCTGCTTATTGAGC 2790764
QY 181 TGAAGAGAGACTGAACCTCAACCTTAAGCATTAAGAGAGCGGTGGCGTCCCAATTGCG 240
Db 2790765 TGAAGAGAGACTGAACCTCAACCTTAAGCATTAAGAGAGCGGTGGCGTCCCAATTGCG 2790824
QY 241 CCACTCCAGCAGCGCAGATCTGATGATCAACAACCTCAAGATAGTATCTTAAGGATAT 300
Db 2790825 CCACTCCAGCAGCGCAGATCTGATGATCAACAACCTCAAGATAGTATCTTAAGGATAT 2790884
QY 301 GTATATCAATATGGAATTCGGGCGTAGAGTATCTGTGAACCGTGCATAAACAGCTGTG 360
Db 2790885 GTATATCAATATGGAATTCGGGCGTAGAGTATCTGTGAACCGTGCATAAACAGCTGTG 2790944
QY 361 ATGAGACTCTTTTCCCTGCAAAAATGTTTTCCAGCGGATGTGAATTTGCGAACCTTGG 420
Db 2790945 ATGAGACTCTTTTCCCTGCAAAAATGTTTTCCAGCGGATGTGAATTTGCGAACCTTGG 2791004
QY 421 TGGCCGCAATTTCAACAGTTGACGCTGCAAAAGCCGCACTCGSCATCGCCACTAGCCCC 480
Db 2791005 TGGCCGCAATTTCAACAGTTGACGCTGCAAAAGCCGCACTCGSCATCGCCACTAGCCCC 2791064
QY 481 GATGATCTCACTGACATATGTAAGTGCCGCTGTGATGAATTTGGCTGCGAATTTG 540
Db 2791065 GATGATCTCACTGACATATGTAAGTGCCGCTGTGATGAATTTGGCTGCGAATTTG 2791124
QY 541 CGATATTTGCTTTCTTCAGGTATGTCACAAAGTGTATCAAGAGTGCAGAGTTGAGCGGT 600
Db 2791125 CGATATTTGCTTTCTTCAGGTATGTCACAAAGTGTATCAAGAGTGCAGAGTTGAGCGGT 2791184
QY 601 GACCTGTGGTATGCGCTGTACTATACGATGTGATATCAGTTGATATACATACATACAT 660
Db 2791185 GACCTGTGGTATGCGCTGTACTATACGATGTGATATCAGTTGATATACATACATACAT 2791244
QY 661 CTTCCCAACATGCGGTGTGAGAGAGAAATGCCGCTCAACGTTTCATGTTGTGGGCA 720
Db 2791245 CTTCCCAACATGCGGTGTGAGAGAGAAATGCCGCTCAACGTTTCATGTTGTGGGCA 2791304
QY 721 GTTGGACACCACTTCTCCAACTGTCTGAGGTTGACCGTTGATCCGTTCCATTCAGGC 780
Db 2791305 GTTGGACACCACTTCTCCAACTGTCTGAGGTTGACCGTTGATCCGTTCCATTCAGGC 2791364
QY 781 TGGTCTACCCCGCTGAGGTGCGGAGAAAATTCGTGACGATGTGAGCAATCGCTGCG 840
Db 2791365 TGGTCTACCCCGCTGAGGTGCGGAGAAAATTCGTGACGATGTGAGCAATCGCTGCG 2791424
QY 841 GTCTTAATGTTTCCCTGTGCGTTGCGTTGGCTGGGCATGATGAGGTGGCGCTGTGCTGT 900
Db 2791425 GTCTTAATGTTTCCCTGTGCGTTGCGTTGGCTGGGCATGATGAGGTGGCGCTGTGCTGT 2791484
QY 901 GCTGTGGGTGGTGAATGGAAGTTTCCCTAATGCTTTTATTAACGGGTTCAAGATCAT 960

Db 2791485 GCTGTGGGTGGTGAATGGAAGTTTCCCTAATGCTTTTATTAACGGGTTCAAGATCAT 2791544
QY 961 TGGCAGACAGTCATTTTGGGAAAGAGGTTTGCTTACCTTCTTCCAAAATGTTGTTGG 1020
Db 2791545 TGGCAGACAGTCATTTTGGGAAAGAGGTTTGCTTACCTTCTTCCAAAATGTTGTTGG 2791604
QY 1021 TGGTTTATTTGCGACGCGCTGCATGATGCTTATTTCTTGGCGTTGCAATTTGGTCT 1080
Db 2791605 TGGTTTATTTGCGACGCGCTGCATGATGCTTATTTCTTGGCGTTGCAATTTGGTCT 2791664
QY 1081 TGAGATCAAAACGAGCCAGATCATGCAATGCAATTTGTTGCTGTGGAGGTTGAC 1140
Db 2791665 TGAGATCAAAACGAGCCAGATCATGCAATGCAATTTGTTGCTGTGGAGGTTGAC 2791724
QY 1141 ACTGTGCAATCTCTGAGAGAGCGCATCAAGGCGCTCCGCTGACAGCAATGACGAT 1200
Db 2791725 ACTGTGCAATCTCTGAGAGAGCGCATCAAGGCGCTCCGCTGACAGCAATGACGAT 2791784
QY 1201 TTTTGAAGAAGCTCCGTTTACCGGCGGCAATTTGCTGGGCGTGGTGGGCAATTCAGCT 1260
Db 2791785 TTTTGAAGAAGCTCCGTTTACCGGCGGCAATTTGCTGGGCGTGGTGGGCAATTCAGCT 2791844
QY 1261 TTCTGAATCTTGCAATGTCAATGTGCTGCAATGAGTCCGCTGCACACCAATTAATTC 1320
Db 2791845 TTCTGAATCTTGCAATGTCAATGTGCTGCAATGAGTCCGCTGCACACCAATTAATTC 2791904
QY 1321 GTCTCAATTTGCCCCGATTTATGCTGTGGCGCTCAACGAGCGGCTTGCAGTGGGTTG 1380
Db 2791905 GTCTCAATTTGCCCCGATTTATGCTGTGGCGCTCAACGAGCGGCTTGCAGTGGGTTG 2791964
QY 1381 TTACGCGGAGTGTGCTCCGCTGATTAATGCGGGGCTTACTGCGCTGATGGGTTCTGGCT 1440
Db 2791965 TTACGCGGAGTGTGCTCCGCTGATTAATGCGGGGCTTACTGCGCTGATGGGTTCTGGCT 2792024
QY 1441 TTATTAATCTTGTGTTTATTTAATTTAGACCCTGCTGCGCGTGCATTCGCAACAGC 1500
Db 2792025 TTATTAATCTTGTGTTTATTTAATTTAGACCCTGCTGCGCGTGCATTCGCAACAGC 2792084
QY 1501 AGTTGGTTTACAGTGTTGTTGCTTCCCGTGCATTTCTGATTCACCGTTGATTTGGC 1560
Db 2792085 AGTTGGTTTACAGTGTTGTTGCTTCCCGTGCATTTCTGATTCACCGTTGATTTGGC 2792144
QY 1561 GATTGCGGCAATCAACCAATGCTTCAGGTCAGAAATTAACGCGGATGTAGACGCAC 1620
Db 2792145 GATTGCGGCAATCAACCAATGCTTCAGGTCAGAAATTAACGCGGATGTAGACGCAC 2792204
QY 1621 CTTGAATGATCAACAATGAGGTTTCAACCAATGCGGTTGCTTTAGCCACTGCTTC 1680
Db 2792205 CTTGAATGATCAACAATGAGGTTTCAACCAATGCGGTTGCTTTAGCCACTGCTTC 2792264
QY 1681 ATCACTTGGCGGTGGGTGTTTGGGTAGTGTGATGCGCGAGGCTACGTGTCACC 1740
Db 2792265 ATCACTTGGCGGTGGGTGTTTGGGTAGTGTGATGCGCGAGGCTACGTGTCACC 2792324
QY 1741 ACGCTTCAACCATACCGCTGATTTACCAAGCGAATGAGTTCTCTTCACGAGGAAC 1800
Db 2792325 ACGCTTCAACCATACCGCTGATTTACCAAGCGAATGAGTTCTCTTCACGAGGAAC 2792384
QY 1801 TGAAGCAATCAAGCGCGCGAGAGAAAAGTCCAAAGACTAATCAAGATTCGTAATTA 1860
Db 2792385 TGAAGCAATCAAGCGCGCGAGAGAAAAGTCCAAAGACTAATCAAGATTCGTAATTA 2792444
QY 1861 AAGGTAAATCAACCTGTTAAGGCGTCTTTCGTTAATACGTAATATCGGGTGA 1920
Db 2792445 AAGGTAAATCAACCTGTTAAGGCGTCTTTCGTTAATATCGTAATATCGGGTGA 2792504
QY 1921 TCGCTTTTAAACACTCAGAGAGATCTTGCAGCGCAAAATCAACGACCTGCCAACCC 1980
Db 2792505 TCGCTTTTAAACACTCAGAGAGATCTTGCAGCGCAAAATCAACGACCTGCCAACCC 2792564
QY 1981 CAGAAATCCCTTACGCTGTTGAAGAGAAACCGACGCGGTGCGGAGATTTGTTGCA 2040

Db	8/8	CTACTTTCTTCCAAAATGTTGTTGGTGGTTTATTATGCGACGGTGCCTGCATCGATTGCTT	93/7
QY	1056	ATTCTTTGGCGTTGCAAATTGTCCTTGAGATCAAAACCGACGCAGATTCAGATCTGGAA	111/5
Db	93/8	ATTCTTTGGCGTTGCAAATTGTCCTTGAGATCAAAACCGACGCAGATTCATCCGATCTGGAA	99/7
QY	1116	TTGTTTGTCGCTTGGCGAGGTTTGACACTTGTCGAATTCCTGCAAGGACGGATCAACGGCGC	117/5
Db	99/8	TTGTTTGTCGCTTGGCGAGGTTTGACAACCTGTCGAATTCCTGCAAGGACGGATCAACGGCGC	105/7
QY	11176	CTCCGGGTGACAGCAATGTCACGATTTTTTGAACAACCTCCTGTTTACCGGCGGCAATTGTTG	123/5
Db	105/8	CTCCGGGTGACAGCAATGTCACGATTTTTTGAACAACCTCCTGTTTACCGGCGGCAATTGTTG	111/7
QY	1236	CTGGCGGTGGGTTTGGGCATTACGCTTTCGAATTTTCATGTCATGATGTTGCTGCTCAATGG	129/5
Db	111/8	CTGGCGGTGGGTTTGGGCATTACGCTTTCGAATTTTCATGTCATGATGTTGCTGCTCAATGG	117/7
QY	1296	AGTCGCGCTGACACCTTAATTATTTGCTCTACATTGCGCCGATTAATGCGTGGTGCGGTCA	135/5
Db	117/8	AGTCGCGCTGACACCTTAATTATTTGCTCTACATTGCGCCGATTAATGCGTGGTGCGGTCA	123/7
QY	1356	CCGACAGCGGCTTCCGACAGGGGTTGTATACGGAGATGGTCTCCGCTATTAATTGGCGGCGC	141/5
Db	123/8	CCGACAGCGGCTTCCGACAGGGGTTGTATACGGAGATGGTCTCCGCTATTAATTGGCGGCGC	129/7
QY	1416	TTACTGCGCTGATGGGTTCTTCGCTTTTATTACTTCCTTCGTGTTTATTATTAAGCCCGCTCT	147/5
Db	129/8	TTACTGCGCTGATGGGTTCTTCGCTTTTATTACTTCCTTCGTGTTTATTATTAAGCCCGCTCT	135/7
QY	1476	CTGCGCGCTGCGAATTGCTGCGCAACAGAGATGGGTTTCACTGGTGGTTTGCTTGCCCTGCAT	153/5
Db	135/8	CTGCGCGCTGCGAATTGCTGCGCAACAGAGATGGGTTTCACTGGTGGTTTGCTTGCCCTGCAT	141/7
QY	1536	TCCTGATTTCACCGTTGATGTTGGCGATGTCGGGCATTCACCAATGCTTCCAGGCTGAG	159/5
Db	141/8	TCCTGATTTCACCGTTGATGTTGGCGATGTCGGGCATTCACCAATGCTTCCAGGCTGAG	147/7
QY	1596	CAATTTCACCGGGGAAATGTAACCCCACTTGATATGATCAAAACATCTGATGGGTTTACCAACA	165/5
Db	147/8	CAATTTCACCGGGGAAATGTAACCCCACTTGATATGATCAAAACATCTGATGGGTTTACCAACA	153/7
QY	1656	TTGCGGTTGCTTTAGCCCACTGCTTCATCACTTGCGCGCTGGCGGTGGTTGGGTAATGGA	171/5
Db	153/8	TTGCGGTTGCTTTAGCCCACTGCTTCATCACTTGCGCGCTGGCGGTGGTTGGGTAATGGA	159/7
QY	1716	TTGCCCCAGGCTTACGTGTCACACCAACCTTCAACCCATACCGTNGATTTTACCAAGGCGA	177/5
Db	159/8	TTGCCCCAGGCTTACGTGTCACACCAACCTTCAACCCATACCGTNGATTTTACCAAGGCGA	165/7
QY	17776	ATGAGTTCCTCTTCCAGAGAGGAAACCTGACAGAAATCAAGCGCGGCGAGAAAACGTCCAA	183/5
Db	165/8	ATGAGTTCCTCTTCCAGAGAGGAAACCTGACAGAAATCAAGCGCGCGAGAAAACGTCCAA	171/7
QY	1836	AGACTTAATCAAGAATTCGGTAATTAAGAATGTAATAATCAACCTGCTTAAAGGAGCTTTCGCT	189/5
Db	171/8	AGACTTAATCAAGAATTCGGTAATTAAGAATGTAATAATCAACCTGCTTAAAGGAGCTTTCGCT	177/7
QY	1896	TAAATTAACGTTAGAAATTCGGGTGATGCTTTTAAACACTACAGAGAAATCCTTGCAGGCC	195/5
Db	177/8	TAAATTAACGTTAGAAATTCGGGTGATGCTTTTAAACACTACAGAGAAATCCTTGCAGGCC	183/7
QY	1956	AAATTAACAGCACTGCTCCACCCCAAGAAATCCCTTCAAGGCTTGAAGAAGAAACCGCA	201/5
Db	183/8	AAATTAACAGCACTGCTCCACCCCAAGAAATCCCTTCAAGGCTTGAAGAAGAAACCGCA	189/7
QY	2016	GCCGGGTG 2022	
Db	189/8	GCCGGGG 1904	

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1 Sequence 3, Application US/09963521
2 Patent No. US20020146781A1
3
4 GENERAL INFORMATION:
5 APPLICANT: ZIEGLER, PETRA
6 APPLICANT: EGGELING, LOTHAR
7 APPLICANT: SAHM, HERMANN
8
9 TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE
10 TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
11 TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
12 FILE REFERENCE: 21123/282413/MAS
13
14 CURRENT APPLICATION NUMBER: US/09/963,521
15
16 PRIOR FILING DATE: 2001-09-27
17 PRIOR APPLICATION NUMBER: 09/431,099
18
19 PRIOR FILING DATE: 1999-11-01
20 PRIOR APPLICATION NUMBER: DE 199 41 478.5
21
22 PRIOR FILING DATE: 1999-09-01
23
24 NUMBER OF SEQ ID NOS: 10
25
26 SOFTWARE: Patentin Ver. 2.1
27
28 SEQ ID NO 3
29
30 LENGTH: 1909
31
32 TYPE: DNA
33
34 ORGANISM: Corynebacterium glutamicum
35
36 FEATURE:
37
38 NAME/KEY: CDS
39
40 LOCATION: (280)..(1746)
41
42 OTHER INFORMATION: thfE-gen
43
44 US-09-963-521-3

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Query Match	65.2%	Score 1836.6	DB 9	Length 1909
Best Local Similarity	99.0%	Pred. No. 0		
Matches 1848; Conservative	0	Mismatches 19	Indels 0	Gaps 0

QY	156	CCCCCTTGACCTGCTGTATATAGCTGGAGAAAGACTTGAACCTCAACCTAGCATTA	211
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QY	216	CAAGTGGCTGACCCCTCCCAATTGGCGCACTCCAGACCGCAATGCTGATGTAACAAC	277
Db	98	CAAGTGGCTGACCCCTCCCAATTGGCGCACTCCAGACCGCAATGCTGATGTAACAAC	15
QY	276	TAGGAATACGTATCTTAGCGTATGTGTACATCAACAAATTCGGGGCTAGATATCTG	335
Db	158	TAGGAATACGTATCTTAGCGTATGTGTACATCAACAAATTCGGGGCTAGATATCTG	21
QY	336	GTGAACCGTGCAAAACGACCTGTATATGATCTCTTTCTCTGTGAAATGTCTTCAAC	395
Db	218	GTGAACCGTGCAAAACGACCTGTATATGATCTCTTTCTCTGTGAAATGTCTTCAAC	27
QY	396	GGATGTGAGTTTGTGACCTTCGTGGCCGCAATTCAAGAGTTGACCGTCCAAAACCG	455
Db	278	GGATGTGAGTTTGTGACCTTCGTGGCCGCAATTCAAGAGTTGACCGTCCAAAACCG	33
QY	456	CACCTCCGCAATGGCACTAGCCCGGATTTGATCTCACTGACCAATAGTCAAGTGGCCG	515
Db	338	CACCTCCGCAATGGCACTAGCCCGGATTTGATCTCACTGACCAATAGTCAAGTGGCCG	397
QY	516	TGATGAATTTGGCTGAGAAATTTGGCAATTTTTCCTTTCCAGTAGTCAACACGTG	575
Db	398	TGATGAATTTGGCTGAGAAATTTGGCAATTTTTCCTTTCCAGTAGTCAACAAATAGTG	457
QY	576	ATACCAAGGTGCAAGTTGAGCGGTGACCTTCGTGTATGGCTGTACTATACCGAATGTG	635
Db	458	ACACCAAGGTGCAAGTTGAGCGGTGACCTTCGTGTATGGCTGTACTATACCGAATGTG	517
QY	636	ATATACCGTTGAATACGATCAACATCTTCAACCAATGTGTGTGAGAGAGAAATGCGG	695
Db	518	ATATACCGTTGAATACGATCAACATCTTCAACCAATGTGTGTGAGAGAGAAATGCGG	577
QY	696	TCAAGGTGTTCAATGTTGGGGCAAGTTGGACACCAACTTCTCCAACTGTCTGAGGTG	755
Db	578	TCAAGGTGTTCAATGTTGTAGGCAAGTTGGACACCAACTTCTCCAACTGTCTGAGGTG	637
QY	756	ACCGTTTATCCGTTCCATTCAGGCTGATGTACCCCGCTGAGGTTGCGGAAATATTC	815

Db 638 ACCGTTGATCCGTTCCATTCAGGCTGAGCGACCCCGCTGAGTTGCGAATAATCC 697
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Qy 1056 ATTCTTTGCGGTTGCAATTTGCTTGAATCAAAACGAGCAGATCATGCTGCTGAA 1115
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Qy 1116 TTGTTGTTGCTGTTGGCGGTTTGACATTTGCGAATCTTGGCAGAGGCGATCACGAGCG 1175
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Qy 1176 CTCGGGAGACGAGAGGACGATTTTGAACACTCTGTTTACGCGCGGCAATGTTG 1235
Db 1058 CTCGGGAGACGAGAGGACGATTTTGAACACTCTGTTTACGCGCGGCAATGTTG 1117
Qy 1236 CTGCGCTGAGGTTTGGGCAATTCAGCTTTCTGAATCTTGCATGTCATGTTGCTGCTGATG 1295
Db 1118 CTGCGCTGAGGTTTGGGCAATTCAGCTTTCTGAATCTTGCATGTCATGTTGCTGCTGATG 1177
Qy 1296 AGTCCGCTGACGACACTTAATTTCTGTACATTCGCGCGGCAATTCGCTGCTGCTGCA 1355
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Db 1298 TTACTGCGCTGATGAGTTCTGCGTTTATTAATCTTTGCTGTTTATTTAGGCCCTGCT 1357
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Qy 1596 CAATTTACGCGGAAATGACGCACTTGAATGATTAACAATCATGCTGCTTCCACCA 1655
Db 1478 CAATTTACGCGGAAATGACGCACTTGAATGATTAACAATCATGCTGCTTCCACCA 1537
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Db 1538 TTGCGGTTGCTTGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1597
Qy 1716 TTGCGCGAGGCTACGCTGCTGCAACAGCTTCAACCCATACGCTGATTTTCCAAAGGCA 1775
Db 1598 TTGCGCGAGGCTACGCTGCTGCAACAGCTTCAACCCATACGCTGATTTTCCAAAGGCA 1657
Qy 1776 ATGAGTTCTCTTCCAGAGAGAACTGAGCAGAAATGAGGCGCGGAGAGAAACGCTCAA 1835
Db 1658 ATGAGTTCTCTTCCAGAGAGAACTGAGCAGAAATGAGGCGCGGAGAGAAACGCTCAA 1717
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Db 1718 AAGCTATTAAGAGATTCGCTTAATAAAGTAAATCAACCTGCTTAAGGCTTTCGCT 1777
Qy 1896 TAAATGCTTAAGATTCGCTGCTGCTTAAACAACCTGAGAGATTCCTGCGGCG 1955
Db 1778 TAAATGCTTAAGATTCGCTGCTGCTTAAACAACCTGAGAGATTCCTGCGGCG 1837
Qy 1956 AAATACAGGACACTGCTGCCAACCAGAAATCCCTTACGCTGTTGAAGAGAAACCGCA 2015
Db 1838 AAATACAGGACACTGCTGCCAACCAGAAATCCCTTACGCTGTTGAAGAGAAACCGCA 1897
Qy 2016 GCCGCTG 2022
Db 1898 GCCGCGG 1904

RESULT 10
US-09-834-721-3
; Sequence 3, Application US/09834721
; Patent No. US2002015551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: PROCESS FOR THE PERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21123/280169/MAS
; CURRENT APPLICATION NUMBER: US/09/834,721
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: DE 100 26 494.8
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: DE 101 02 823.7
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC13032
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
; OTHER INFORMATION: thre gene
US-09-834-721-3

Query Match 65.2%; Score 1836.6; DB 9; Length 1909;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 156 CCCCTTTACCTGCTGTTATTTAGCTGAGAGAGACTTGAACCTCAACCTACCATTA 215
Db 38 CCCCTTTACCTGCTGTTATTTAGCTGAGAGAGACTTGAACCTCAACCTACCATTA 97
Qy 216 CAAGTGCCTGGCTGCCAATTTGCCCACTCCAGACCGCAGATGCTGATCAACAG 275
Db 98 CAAGTGCCTGGCTGCCAATTTGCCCACTCCAGACCGCAGATGCTGATCAACAG 157
Qy 276 TAGCAATACGTAATCTTAGCGATGTTGTACATACATGAAATGGGGCTAGAGATCTG 335
Db 158 TAGCAATACGTAATCTTAGCGATGTTGTACATACATGAAATGGGGCTAGAGATCTG 217
Qy 336 GTGAACCGGATTAACAGACCTGATGAGACTCTTTTCTTGGCAAAATGTTTCCAGC 395
Db 218 GTGAACCGGATTAACAGACCTGATGAGACTCTTTTCTTGGCAAAATGTTTCCAGC 277
Qy 396 GGAATGTAATTTTGGCAACCTTCTGAGCGGATTTCAACAGTTGACGCTGCAAAAGCGG 455
Db 278 GGAATGTAATTTTGGCAACCTTCTGAGCGGATTTCAACAGTTGACGCTGCAAAAGCGG 337
Qy 456 CACCTTCGCGCATGCGCACTAGCGCCGATGATCTCAACATATCAAGTCAAGTCCGCGTG 515
Db 338 CACCTTCGCGCATGCGCACTAGCGCCGATGATCTCAACATATCAAGTCAAGTCCGCGTG 397
Qy 516 TGAATGATTTGGCTGAGAGATTTGGGATATTTGCTTTCTTCAAGTCAAGTCAAGT 575
Db 398 TGAATGATTTGGCTGAGAGATTTGGGATATTTGCTTTCTTCAAGTCAAGTCAAGT 457

Db 218 GTGAACCGTGCAATAAGACCTGTGATTGGACTCTTTCTTGCAAAATGTTTCCAG 277
 QY 396 GGATGTTGAGTTTGGACCTTCTGTGCGCAATTTCAACATGTGACGTGCAAAACCG 455
 Db 278 GGATGTTGAGTTTGGACCTTCTGTGCGCAATTTCAACATGTGACGTGCAAAACCG 337
 QY 456 CACCTCGGCATGCGCATGTGCCCCGATTGATCTCACTGACCAATGATCAAGTGGCCGGT 515
 Db 338 CACCTCGGCATGCGCATGTGCCCCGATTGATCTCACTGACCAATGATCAAGTGGCCGGT 397
 QY 516 TGAATGATTTGGCTGCGAGAAATGGCGATTTTGTGCTTCTCAGTACGTCAAAACAGT 575
 Db 398 TGAATGATTTGGCTGCGAGAAATGGCGATTTTGTGCTTCTCAGTACGTCAAAACAGT 457
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 Db 518 ATATCAGTGTGAATGATGATCAACCATCTTCAACCAATCGGTTGGAGAGAGATGCGCG 577
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 Db 578 TCAACGTTTCAATGTTGGGCAAGTTGACACCAACTTCTCCAACTGTCTGAGTTG 637
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 QY 996 CTACTTTCTTCAAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1055
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 Db 1178 AGTCCGCTGACAGCACTTAATTTATGCTCTACATTTGCGCGCATTCAGTGTG 1237
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QY 1476 CTGCGCTGCGATTTGCTGCAACAGCAGTTGTTTCACTGTGTGTTGCTTGCCTGCGAT 1535
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 QY 1596 CAATTTACCGCGGAATGACCGCATTCGATGATGATCAACACTCATGGTTTCAACACA 1655
 Db 1478 CAATTTACCGCGGAATGACCGCATTCGATGATGATCAACACTCATGGTTTCAACACA 1537
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 QY 1896 TAAATAGCGTAATATTCGGGTGATGCTTTTAAACATCAGAGAGATTCCTGCGCGC 1955
 Db 1778 TAAATAGCGTAATATTCGGGTGATGCTTTTAAACATCAGAGAGATTCCTGCGCGC 1837
 QY 1956 AAATTCACGAGCATCTGCTCCACCCAGAAATCCCTTCAAGCTGTGTGAAGAGAAACCGCA 2015
 Db 1838 AAATTCACGAGCATCTGCTCCACCCAGAAATCCCTTCAAGCTGTGTGAAGAGAAACCGCA 1897
 QY 2016 GCCGGTG 2022
 Db 1898 GCCGGTG 1904

RESULT 12
 US-09-951-535-3
 ; Sequence 3, Application US/09951535
 ; Publication No. US2003049802A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZIEGLER, PETRA
 ; APPLICANT: EGGELING, LOTHAR
 ; APPLICANT: SAHM, HERMANN
 ; APPLICANT: THIERBACH, GEORG
 ; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
 ; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
 ; TITLE OF INVENTION: USING CORYNEFORM BACTERIA
 ; FILE REFERENCE: 21123/282415/MAS
 ; CURRENT APPLICATION NUMBER: US/09/951,535
 ; PRIOR FILING DATE: 2001-09-14
 ; PRIOR APPLICATION NUMBER: 09/431,099
 ; PRIOR FILING DATE: 1999-11-01
 ; PRIOR APPLICATION NUMBER: DE 199 41 478.5
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patencin Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 1909
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (280)..(1746)
 ; OTHER INFORMATION: three-Gen
 US-09-951-535-3

Query Match 65.2%; Score 1836.6; DB 10; Length 1909;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 156 CCCCTTTGACCTGATGTTATGAGCTGGAAGAAGACTTGAACCTGCAACCTGACCATTA 215
 Db CCCCTTTGACCTGATGTTATGAGCTGGAAGAAGACTTGAACCTGCAACCTGACCATTA 97
 QY 216 CAAGTGCCTTGGCGCTGCGCAATTGGCGCACTCCAGACCGGACGATGATGATCAAC 275
 Db CAAGTGCCTTGGCGCTGCGCAATTGGCGCACTCCAGACCGGACGATGATGATCAAC 157
 QY 276 TACGAATACGATCTTAGCGATGATGATCATCAAGATGGAATGGGGCTGAGATCTG 335
 Db TACGAATACGATCTTAGCGATGATGATCATCAAGATGGAATGGGGCTGAGATCTG 217
 QY 336 GTGAACCGTGCAATAACGACCTGATGATGACTCTTTTCTTTGCAAAATGTTTCCAGC 395
 Db GTGAACCGTGCAATAACGACCTGATGATGACTCTTTTCTTTGCAAAATGTTTCCAGC 277
 QY 396 GGATGTTGAGTTTGGCCGACCTTGTGGCGGCATTTCAAGATTGACGCTGCAAAAGCG 455
 Db GGATGTTGAGTTTGGCCGACCTTGTGGCGGCATTTCAAGATTGACGCTGCAAAAGCG 337
 QY 456 CACCTCGGCATGCGCACTAGCCCGATGATGATCACTGACGACATGATCAAGTGGCGG 515
 Db CACCTCGGCATGCGCACTAGCCCGATGATGATCACTGACGACATGATCAAGTGGCGG 397
 QY 516 TGATGAATTTGGCTGCGAGAAATGGCGATATTTTGTCTTCTCAGTACGTCAAACAGTG 575
 Db TGATGAATTTGGCTGCGAGAAATGGCGATATTTTGTCTTCTCAGTACGTCAAACAGTG 457
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 QY 636 ATATACGCTGAATACGATACCACTTCTCAACCAATCGGTGTGAGAGAGAAATGTCGG 695
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 QY 756 ACCGTTGATCCGTTTCCATTCAAGCTGTGTCTACCCCGCTGAGGTTCCGAGAAAATTC 815
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 Db CTACTTCTTCCAAATGTTGTGGGTTTATTTGCGACGCGCTGATGATGCTT 937
 QY 1056 ATTCTTTGGCGTTGCAATTTGCTTTGAGATCAACCGAGCCAGATCATCGATCTGGA 1115
 Db ATTCTTTGGCGTTGCAATTTGCTTTGAGATCAACCGAGCCAGATCATCGATCTGGA 997
 QY 1116 TTGTTGTGTTGAGAGGTTTGAACCTTTGTCATCTTGAAGACGGCATACGGGGC 1175
 Db TTGTTGTGTTGAGAGGTTTGAACCTTTGTCATCTTGAAGACGGCATACGGGGC 1057
 QY 1176 CTCGCGTGAACAGAGTGCAGATTTTGAAGAACTCCTGTTTACCGGCGCATTTGTTG 1235

Db 1058 CTCGCGTGAACAGAGTGCAGATTTTGAAGAACTCCTGTTTACCGGCGCATTTGTTG 1117
 QY 1236 CTGGGTTGGGTTTGGGCAATTGAGCTTTGAAATCTGATGTCAATGTTGCTGCAATG 1295
 Db CTGGGTTGGGTTTGGGCAATTGAGCTTTGAAATCTGATGTCAATGTTGCTGCAATG 1177
 QY 1296 AGTCGCTGAGACCTTAATTTGCTAATTTGCCCCGATTAATGCTGTGGCTGTCA 1355
 Db AGTCGCTGAGACCTTAATTTGCTAATTTGCCCCGATTAATGCTGTGGCTGTCA 1237
 QY 1356 CCGAGCGGCTTGCAGTGGGTTTGAACGGAGTGTCTCGGTGATTAATTTGAGGGAGC 1415
 Db CCGAGCGGCTTGCAGTGGGTTTGAACGGAGTGTCTCGGTGATTAATTTGAGGGAGC 1297
 QY 1416 TTACTGCGCTATGAGGTTCTGCGTTTATTAACCTCTTGTGTTATTTAAGCCCCGTCT 1475
 Db TTACTGCGCTATGAGGTTCTGCGTTTATTAACCTCTTGTGTTATTTAAGCCCCGTCT 1357
 QY 1476 CTGCGGCTGCGATGCTGCAACAGACGTTGTTCACTGTGTGTTTGTGCTTCCGAT 1535
 Db CTGCGGCTGCGATGCTGCAACAGACGTTGTTCACTGTGTGTTTGTGCTTCCGAT 1417
 QY 1536 TCTTATTCACCGCTTATTTGTGCGATTGGCGGATCAACCAATGCTTCCAGTCTAG 1595
 Db TCTTATTCACCGCTTATTTGTGCGATTGGCGGATCAACCAATGCTTCCAGTCTAG 1477
 QY 1596 CAATTTACCGCGGAATGTAAGCCACCTTGAATGATCAAAACATCTAGTGGTTTCCACAA 1655
 Db CAATTTACCGCGGAATGTAAGCCACCTTGAATGATCAAAACATCTAGTGGTTTCCACAA 1537
 QY 1656 TTGCGGTTGCTTAGCCACTGCTTCACTCTGCGGTGGCGTGTGTTGGGTGAGTGA 1715
 Db TTGCGGTTGCTTAGCCACTGCTTCACTCTGCGGTGGCGTGTGTTGGGTGAGTGA 1597
 QY 1716 TTGCGCGAGGCTTACGTCGTCACACGCTTCAACCATACCTGCAATTTACCAAGGCGA 1775
 Db TTGCGCGAGGCTTACGTCGTCACACGCTTCAACCATACCTGCAATTTACCAAGGCGA 1657
 QY 1776 ATGAGTTCTCTTCCAGAGGAAAGCTGAGCAATGACGCGCGGACAGAAAAGTCCAA 1835
 Db ATGAGTTCTCTTCCAGAGGAAAGCTGAGCAATGACGCGCGGACAGAAAAGTCCAA 1717
 QY 1836 AGACTAATCAAAATTCGGAATTAAGGTAAGTAATCAACCTAGAGGCTCTTTCGCT 1895
 Db AGACTAATCAAAATTCGGAATTAAGGTAAGTAATCAACCTAGAGGCTCTTTCGCT 1777
 QY 1896 TAAATGCGTAAGATTCGAGTGCATGCTTTTAAACACTCAGAGAGATCTTCCGCGC 1955
 Db TAAATGCGTAAGATTCGAGTGCATGCTTTTAAACACTCAGAGAGATCTTCCGCGC 1837
 QY 1956 AAAATCAGGACACTGTCGCCACCCGAGAAATCCCTTCAAGCTGTGTAAGAGAAACGCA 2015
 Db AAAATCAGGACACTGTCGCCACCCGAGAAATCCCTTCAAGCTGTGTAAGAGAAACGCA 1897
 QY 2016 GCCGGTG 2022
 Db 1898 GCCGGG 1904

RESULT 13
 US-10-224-574-11
 ; Sequence 11, Application US/10224574
 ; Publication No. US20040101837A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Forschungszentrum Jlich GmbH, P. Ziegler, L. Eggeling, H. Sahn,
 ; APPLICANT: P. Peters-Wendisch
 ; TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the syn
 ; TITLE OF INVENTION: L-Serin, improved process for the microbial manufacture of L-ser
 ; FILE REFERENCE: FZJ-9912-PCT
 ; CURRENT APPLICATION NUMBER: US/10/224, 574
 ; CURRENT FILING DATE: 2002-08-21

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/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO. 11
/ LENGTH: 1909
/ TYPE: DNA
/ ORGANISM: C. glutamicum ATCC 13 032
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (280)..(1746)
/ OTHER INFORMATION: thr E (Threonine-exportcarrier)
US-10-224-574-11

Query Match      65.2%; Score 1836.6; DB 17; Length 1909;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 156 CCCCTTGACCTGGTGTATTTAGAGCTGAGAGAGACTTGAACCTCAACCTACGCACTTA 215
Db 38 CCCCTTGACCTGGTGTATTTAGAGCTGAGAGAGACTTGAACCTCAACCTACGCACTTA 97

QY 216 CAAGTGGCTTGCGCTGCCAATTGGCCCACTCCAGCACCGGAGATGTGATGATCAACAC 275
Db 98 CAAGTGGCTTGCGCTGCCAANTGGCCCACTCCAGCACCGGAGATGTGATGATCAACAC 157

QY 276 TACGAATACGTATCTTAGCGTATGTGATCATCAACAATGGAATTGGGGCTTAGATATCTG 335
Db 158 TACGAATACGTATCTTAGCGTATGTGATCATCAACAATGGAATTGGGGCTTAGATATCTG 217

QY 336 GTGAACCGCTGATMAAGAGACCTGTGATGAGACTCTTTTCTCTGCAAAATGTTTCAGC 395
Db 218 GTGAACCGCTGATMAAGAGACCTGTGATGAGACTCTTTTCTCTGCAAAATGTTTCAGC 277

QY 396 GGATGTGAGTTTGCGACACCTCTGTGGCCGCAATTTCAACAGTTGACGCTGCAAAAGCGG 455
Db 278 GGAATGTGAGTTTGCGACACCTCTGTGGCCGCAATTTCAACAGTTGACGCTGCAAAAGCGG 337

QY 456 CACCTCCGCATCCGCACTAGCCCCGATTTGATCTCACTGACCAATGTAAGAGGCCGGTG 515
Db 338 CACCTCCGCATCCGCACTAGCCCCGATTTGATCTCACTGACCAATGTAAGAGGCCGGTG 397

QY 516 TGATCAATTTGGCTGCGAGAAATGGCGAATTTTCTTCTTCAGAGTCAACAACAGTG 575
Db 398 TGATCAATTTGGCTGCGAGAAATGGCGAATTTTCTTCTTCAGAGTCAACAATGAGTG 457

QY 576 ATACCAAGTGAATTCGAGCGGTGACCTCTGCGTATGACCTGTACTATACGCAATG 635
Db 458 ATACCAAGTGAATTCGAGCGGTGACCTCTGCGTATGACCTGTACTATACGCAATG 517

QY 636 ATATCACTGTAATACGATACCAATCTTCAACCAATCGGTGTGAGAGAGATGCCGG 695
Db 518 ATATCACTGTAATACGATACCAATCTTCAACCAATCGGTGTGAGAGAGATGCCGG 577

QY 696 TCAAGTGTTCATGTTGGGCAAGTTGGACACCAACTTCTCAAACTGTCTGAGTTG 755
Db 578 TCAAGTGTTCATGTTGGGCAAGTTGGACACCAACTTCTCAAACTGTCTGAGTTG 637

QY 756 ACCGTTTGAATCCGTTCCATTCAGGCTGAGTCTGACCCCGCTGAGGTTGCCGGAATTC 815
Db 638 ACCGTTTGAATCCGTTCCATTCAGGCTGAGTCTGACCCCGCTGAGGTTGCCGGAATTC 697

QY 816 TGGAGAGATTGAGACCAATGCCCTGCTTATGAGTTTCCGTGTGCGTGGCTGG 875
Db 698 TGGAGAGATTGAGACCAATGCCCTGCTTATGAGTTTCCGTGTGCGTGGCTGG 757

QY 876 CAATGATGGGTGGCGCTGTGCTGTGTGAGGTGAGATGGCAAGTTTCCCTAATTG 935
Db 758 CAATGATGGGTGGCGCTGTGCTGTGTGAGGTGAGATGGCAAGTTTCCCTAATTG 817

QY 936 CTTTATTTACCGGTTTACGATCATTTGCCACGATCATTTTGGGAAAGAGGGTTTGC 995
Db 818 CTTTATTTACCGGTTTACGATCATTTGCCACGATCATTTTGGGAAAGAGGGTTTGC 877

QY 996 CTAATTTCTTCCAAATGTTTGTGTGTTTATTCACAGCGTGCATGATGCTT 1055
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Db 878 CTAATTTCTTCCAAATGTTTGTGTGTTTATTCACAGCGTGCATGATGCTT 937
QY 1056 ATTCTTTGGCGTTTGCAATTTGGCTTGTAGATCAAAACGAGCCGAGATCATGATCGAA 1115
Db 938 ATTCTTTGGCGTTTGCAATTTGGCTTGTAGATCAAAACGAGCCGAGATCATGATCGAA 997

QY 1116 TTGTGTGCTGTGTGGAGGTTTGACACTTGTGCATCTCTGCAAGAGCGGATCAAGGCG 1175
Db 998 TTGTGTGCTGTGTGGAGGTTTGACACTGCTGTGCATCTCTGCAAGAGCGGATCAAGGCG 1057

QY 1176 CTCGGTGACAGCAAGTGACAGATTTTGTGAACAACCTCTGTTTACCGGGCGCATTTG 1235
Db 1058 CTCGGTGACAGCAAGTGACAGATTTTGTGAACAACCTCTGTTTACCGGGCGCATTTG 1117

QY 1236 CTGGCGTGGTTTGGGATTCAGCTTTCGAATTCGTGATCATGTTGCTCCGCAATG 1295
Db 1118 CTGGCGTGGTTTGGGATTCAGCTTTCGAATTCGTGATCATGTTGCTCCGCAATG 1177

QY 1296 AGTCCGCTGACAGCACTAATTAATTCGTACTATTCGCCGCAATTATGCTGTGGCTCA 1355
Db 1178 AGTCCGCTGACAGCACTAATTAATTCGTACTATTCGCCGCAATTATGCTGTGGCTCA 1237

QY 1356 CCGCAGCGGCTTTCGACGTGGTTTACGCGAGTGTCTCTGGTGTATTTAGCGGGGC 1415
Db 1238 CCGCAGCGGCTTTCGACGTGGTTTACGCGAGTGTGTCTCTGGTGTATTTAGCGGGGC 1297

QY 1416 TTACTGTGCTGATGGGTTTCCGCTTATTAACCTCTGTTGTTATTTAGGCCCGCT 1475
Db 1298 TTACTGTGCTGATGGGTTTCCGCTTATTAACCTCTGTTGTTATTTAGGCCCGCT 1357

QY 1476 CTGCGCTGACGATTTGCTGCAACAGCAGTGGTTTCACTGTGTGTTTGTCCCGTGAT 1535
Db 1358 CTGCGCTGACGATTTGCTGCAACAGCAGTGGTTTCACTGTGTGTTTGTCCCGTGAT 1417

QY 1536 TCTTGATTCACCGTTGATTTGTGGCATTTGCCGCAATACCAATGCTTCAGGTCTAG 1595
Db 1418 TCTTGATTCACCGTTGATTTGTGGCATTTGCCGCAATACCAATGCTTCAGGTCTAG 1477

QY 1596 CAATTTACCGGGGAATGATGAGCCACCTGATGATCAACAACCTAGGTTTCAACAA 1655
Db 1478 CAATTTACCGGGGAATGATGAGCCACCTGATGATCAACAACCTAGGTTTCAACAA 1537

QY 1656 TTGCGGTTGTTTGAAGCACTGCTTCATCACTTCCGCTGGCGGTGTTTGGGTGATGA 1715
Db 1538 TTGCGGTTGTTTGAAGCACTGCTTCATCACTTCCGCTGGCGGTGTTTGGGTGATGA 1597

QY 1716 TTGCCGAGGCTACGTGTCTCAACAGCTTCAACCAATACCGTGCATTTACCAAGCGA 1775
Db 1598 TTGCCGAGGCTACGTGTCTCAACAGCTTCAACCAATACCGTGCATTTACCAAGCGA 1657

QY 1776 ATGATGTTCTCTTCAGAGGAGAGCTGAGCAATACAGGCGGGGAGAGAAACGTCAA 1835
Db 1658 ATGATGTTCTCTTCAGAGGAGAGCTGAGCAATACAGGCGGGGAGAGAAACGTCAA 1717

QY 1836 AGACTAATCAAGATTCGGTAATAAAGGTAAAAATCAACCTGCTTAAAGCGCTTTGGT 1895
Db 1718 AGACTAATCAAGATTCGGTAATAAAGGTAAAAATCAACCTGCTTAAAGCGCTTTGGT 1777

QY 1896 TAAATAGCGTAAATATCGGGTGCATCGCTTTTAAACATCGAGAGATCTTTGCCGGC 1955
Db 1778 TAAATAGCGTAAATATCGGGTGCATCGCTTTTAAACATCGAGAGATCTTTGCCGGC 1837

QY 1956 AAAATCAAGGACACTGTCACCAACCCAGAGATCCCTTCAAGCTGTGTAAGAGAAACGCA 2015
Db 1838 AAAATCAAGGACACTGTCACCAACCCAGAGATCCCTTCAAGCTGTGTAAGAGAAACGCA 1897

QY 2016 GCCGGTG 2022
Db 1898 GCCGGG 1904
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RESULT 14

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US-10-627-476-557
; Sequence 557, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGT-125CPCN
; CURRENT APPLICATION NUMBER: US/10/627,476
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 557
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXN00349
US-10-627-476-557

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Query Match	55.4%	Score 1561.2	DB 13	Length 1590
Best Local Similarity	98.9%	Pred. No. 0		
Matches 1572	Conservative	0	Mismatches 18	Indels 0
				Gaps 0
QY	298	TGTTACTATCAATGSAATCGGGGGCTAGAGTATCTGGTGAACCGTGCATTAACGACT	357	
Db	1	TGTGTACATCAATGSAATCGGGGCTAGAGTATCTGTGAACCGTGCATTAACGACT	60	
QY	358	GTGATTTGACCTCTTTTCCCTTGCAGAAATGTTTTCCAGCGGATGTGAGTTTGGACCCCT	417	
Db	61	GTGATTTGACCTCTTTTCCCTTGCAGAAATGTTTTCCAGCGGATGTGAGTTTGGACCCCT	120	
QY	418	TCGTGGCCGCAATTTCAACAGTTGAOGCTGCAAAAGCCGACCTCGCATCGCACTAGC	477	
Db	121	TCGTGGCCGCAATTTCAACAGTTGAOGCTGCAAAAGCCGACCTCGCATCGCACTAGC	180	
QY	478	CCCGATTTGATCTCACTGACCACTAGTCAAAGTGGCGGTGTGTGTAATTTGGCTGCGAGAT	537	
Db	181	CCCGATTTGATCTCACTGACCACTAGTCAAAGTGGCGGTGTGTGTAATTTGGCTGCGAGAT	240	
QY	538	TGGGATATTTTGGTTCTTCAAGTAGTCAAACAGTGATACCAAGTGCAGTTGACG	597	
Db	241	TGGGATATTTTGGTTCTTCAAGTAGTCAAACAGTGATACCAAGTGCAGTTGACG	300	
QY	598	GGTACCTCTGCGATGAGCTGTACTATAGCGATGTGGATATCACTTTGAATAGATCAC	657	

Db	301	AGTGAACCTCGGTGATGAGTTTGATCTACACGACAGCTGGATATACAGTTGAATACATACAC	360
QY	658	CATCTTACCAACATCGGTGTGTGAGAGAGAAAGATGCGGTCAACGTTTCATGTTGTAGG	717
Db	361	CATCTTACCAACATCGGTGTGTGAGAGAGAAAGATGCGGTCAACGTTTCATGTTGTAGG	420
QY	718	CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGTTGACCGTTTGATCCGTTCAATTCA	777
Db	421	CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGTTGACCGTTTGATCCGTTCAATTCA	480
QY	778	GGCTGTGTGTACCCCGCCCTGAGAGTTGCCGAGAAATTCCTGACAGAGTTGGACATCGCC	837
Db	481	GGCTGTGTGTACCCCGCCCTGAGAGTTGCCGAGAAATTCCTGACAGAGTTGGACATCGCC	540
QY	838	TGCGTCTTAATGATTTCCCTGTGCGCTGTTGGCTGGCAATGATAGAGGTGGCGTGTGC	897
Db	541	TGCGTCTTAATGATTTCCCTGTGTGCGCTGTTGGCTGGCAATGATAGAGGTGGCGTGTGC	600
QY	898	TGTGCTGTTGGGTGGTGGATGAGCAGAGTTCCCTAAATGCTTTATTAACGCGCTTCACAT	957
Db	601	TGTGCTGTTGGGTGGTGGATGAGCAGAGTTCCCTAAATGCTTTATTAACGCGCTTCACAT	660
QY	958	CATTCGCACGAGCTATTTTGGGAAAAGAGGTTTGCTTACTTTCTTCCAAATGTTGT	1017
Db	661	CATTCGCACGAGCTATTTTGGGAAAAGAGGTTTGCTTACTTTCTTCCAAATGTTGT	720
QY	1018	TGGTGGTTTAAATTTGCGACGCTCCCGACATTCCTAATCTTGGGGGTTGCAATTTGG	1077
Db	721	TGGTGGTTTAAATTTGCGACGCTCCCGACATTCCTAATCTTGGGGGTTGCAATTTGG	780
QY	1078	TTTTSAGATCAAAACCGAGCCAGATCATCGACTTGGAAATGTTGTGCTGTGGCAGGTTT	1137
Db	781	TTTTSAGATCAAAACCGAGCCAGATCATCGACTTGGAAATGTTGTGCTGTGGCAGGTTT	840
QY	1138	GACACTTGTGCAATCTCTGACAGAGAGATCAACGGGCGCTCCGTTGACAGCAAGTCACG	1197
Db	841	GACACTTGTGCAATCTCTGACAGAGAGATCAACGGGCGCTCCGTTGACAGCAAGTCACG	900
QY	1198	ATTTTGTGAAACACTCTCTGTTTACCGGCGGCGATTTGTTCTGCGCGGTTTGGCGATTCA	1257
Db	901	ATTTTGTGAAACACTCTCTGTTTACCGGCGGCGATTTGTTCTGCGCGGTTTGGCGATTCA	960
QY	1258	GCTTCTGAAATCTTGCAATGTCATGTTGCTGCGCATGAGAGTCCGCTGAGCACTTAATTA	1317
Db	961	GCTTCTGAAATCTTGCAATGTCATGTTGCTGCGCATGAGAGTCCGCTGAGCACTTAATTA	1020
QY	1318	TTTGTGCTACATTTGCCCGCATTAATTCGCTGTGTGGGTCAACGCGACGGCTTTCGACGTGGG	1377
Db	1021	TTTGTGCTACATTTGCCCGCATTAATTCGCTGTGTGGGTCAACGCGACGGCTTTCGACGTGGG	1080
QY	1378	TTTGTACCGGAGAGTGTCTCGGTGATTAATTTGCGGGGCTTACGTGCGCATAGGGTTCTGC	1437
Db	1081	TTTGTACCGGAGAGTGTCTCGGTGATTAATTTGCGGGGCTTACGTGCGCATAGGGTTCTGC	1140
QY	1438	GTTTAAATTAACCTCTGTGTGTTTAAATTTAGGCCCGCTCTGCGCGCTGCAATTCGTGCAAC	1497
Db	1141	GTTTAAATTAACCTCTGTGTGTTTAAATTTAGGCCCGCTCTGCGCGCTGCAATTCGTGCAAC	1200
QY	1498	AGCAGTTGGTTTACCTGAGTGTGTTGTTGCCCGCTGCATTTCTTAATTCACCGTTGATGT	1557
Db	1201	AGCAGTTGGTTTACCTGAGTGTGTTGTTGCCCGCTGCATTTCTTAATTCACCGTTGATGT	1260
QY	1558	GGCAGATTCGCGGCACTACACCAATGCTTCCAGGCTGAGCAATTTACCGCGGAATGTACGC	1617
Db	1261	GGCAGATTCGCGGCACTACACCAATGCTTCCAGGCTGAGCAATTTACCGCGGAATGTACGC	1320
QY	1618	CACCTTGAATGATCAAACTCTATGAGTTTACCAACATTTGCGGTTGCTTTAGCACTGC	1677
Db	1321	CACCTTGAATGATCAAACTCTATGAGTTTACCAACATTTGCGGTTGCTTTAGCACTGC	1380
QY	1678	TTTATACCTTGGCGGCTGGGTGTTTGGGTGATGTGATTCGCCGACGCTACGTCGTCC	1737
Db	1381	TTTATACCTTGGCGGCTGGGTGTTTGGGTGATGTGATTCGCCGACGCTACGTCGTCC	1440

Query 1738 ACCAGCTTCAACCCATACCGTGCATTTACCAAGGCAATGATGTTCTTCTTCCAGAGGA 1797
Db 1441 ACCAGCTTCAACCCATACCGTGCATTTACCAAGGCAATGATGTTCTTCTTCCAGAGGA 1500
QY 1798 AGCTGACACAAATCAGGCGCGGACAGAAAAAGTCCAAAGACTAATCAAGATTGCGTAA 1857
Db 1501 AGCTGACACAAATCAGGCGCGGACAGAAAAAGTCCAAAGACTAATCAAGATTGCGTAA 1560
QY 1858 TAAAGGTAAATAATCAACTGCTTAAAGCGT 1887
Db 1561 TAAAGGTAAATAATCAACTGCTTAAAGCGT 1590

RESULT 15
US-10-450-055-41
Sequence 41, Application US/10450055
Publication No. US20040043953A1
GENERAL INFORMATION:
APPLICANT: BASF Aktiengesellschaft
TITLE OF INVENTION: No. US20040043953A1 genes of Corynebacterium
FILE REFERENCE: 936 2000
CURRENT APPLICATION NUMBER: US/10/450,055
CURRENT FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Vers. 2.0
SEQ ID NO 41
LENGTH: 1590
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1567)
OTHER INFORMATION: RXS00349
US-10-450-055-41

Query Match 55.4%; Score 1561.2; DB 13; Length 1590;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 298 TGTGTACATCAAAAGAAATCGGGCTAGAGTATCTGTGTAACCGTGCATTAACGACCT 357
Db 1 TGTGTACATCAAAAGAAATCGGGCTAGAGTATCTGTGTAACCGTGCATTAACGACCT 60

QY 358 GTGATTTGAATCTTTTCTTCTTCCAAAATGTTTTCCAGCGAGTGTGATTTGGCGACCT 417
Db 61 GTGATTTGAATCTTTTCTTCTTCCAAAATGTTTTCCAGCGAGTGTGATTTGGCGACCT 120

QY 418 TGTGTGCGGCAATTTCAAGAGTTGAGCGCTGCAAAAGCCGACCTCCGCACTCCGCACTAGC 477
Db 121 TGTGTGCGGCAATTTCAAGAGTTGAGCGCTGCAAAAGCCGACCTCCGCACTCCGCACTAGC 180

QY 478 CCCGATTGATCTCACTGACCATAGTCAGTGGCCGCTGTGATGAATTTG3CTGCGAAT 537
Db 181 CCCGATTGATCTCACTGACCATAGTCAGTGGCCGCTGTGATGAATTTG3CTGCGAAT 240

QY 538 TGGCGAATTTTCTTCTTCTTCCAGTACGTTCAACATGATACCAAGTGCAGATTGAGC 597
Db 241 TGGCGAATTTTCTTCTTCTTCCAGTACGTTCAACATGATACCAAGTGCAGATTGAGC 300

QY 598 GGGAGCTCTGCGATAGCGCTGACTATAAGCATGTGATATCAAGTTGATATGATCAC 657
Db 301 AGTGACCTCTGCGATAGCGCTGACTATAAGCATGTGATATCAAGTTGATATGATCAC 360

QY 658 CATCTTCAACCAATCGGTGTGAGAGGAAGATGCGGTCAACGTTTCAATGTTGAG 717
Db 361 CATCTTCAACCAATCGGTGTGAGAGGAAGATGCGGTCAACGTTTCAATGTTGAG 420

QY 718 CAAAGTGAACCAATCTTCCAAACGTCTGAGTTGACCGTTGATCCGTTCCATTA 777
Db 421 CAAAGTGAACCAATCTTCCAAACGTCTGAGTTGACCGTTGATCCGTTCCATTA 480

QY 778 GCGTGTGTACCCCGCTAGAGTTGCCGAGAAAATTTGAGACAGTTGAGCAATCGCC 837

Db 481 GCGTGTGTACCCCGCTAGAGTTGCCGAGAAAATCTTGAACGAGTTGAGCAATCC 540
QY 838 TGGCTCTTAATGTTTCCCTTGTGTTGCTTGGCTGGGCAATGATGAGTGGCGCTTGGC 897
Db 541 TGGCTCTTAATGTTTCCCTTGTGTTGCTTGGCTGGGCAATGATGAGTGGCTTGGC 600
QY 898 TGTGCTGTGGGTGGTGGATGAGGAGTTTCCCTAATTTGCTTTAATTAACCGGTTACGAT 957
Db 601 TGTGCTGTGGGTGGTGGATGAGGAGTTTCCCTAATTTGCTTTAATTAACCGGTTACGAT 660
QY 958 CATTTGCCAGACGTCATTTTGGGAAAGAGGTTTGGCTAATCTTCCAAATGTTGT 1017
Db 661 CATTTGCCAGACGTCATTTTGGGAAAGAGGTTTGGCTAATCTTCCAAATGTTGT 720

QY 1018 TGTGTTTATTAATGCGACGCTGCTGATGATGCTTATTTCTTGGCGTTGCAATTTG 1077
Db 721 TGTGTTTATTAATGCGACGCTGCTGATGATGCTTATTTCTTGGCGTTGCAATTTG 780

QY 1078 TCTTGAGATCAAAACCGACGATCATGCAATGCAATGTTGTGCTGTGGCAGGTTT 1137
Db 781 TCTTGAGATCAAAACCGACGATCATGCAATGCAATGTTGTGCTGTGGCAGGTTT 840

QY 1138 GACACTTGTGCAATCTTGTGCGAGACGCGATTCACGGGCGCTCCGTTGACAGAGTGCAG 1197
Db 841 GACACTTGTGCAATCTTGTGCGAGACGCGATTCACGGGCGCTCCGTTGACAGAGTGCAG 900

QY 1198 ATTTTGTGAAACACCTCCGTTTACCGGCGGATTTGCTG3CGGTG3GTTTGGCATTA 1257
Db 901 ATTTTGTGAAACACCTCCGTTTACCGGCGGATTTGCTG3CGGTG3GTTTGGCATTA 960

QY 1258 GCTTCTGAAATCTTGCAATGTCATGTTGCTGCAATGAGTGCCTGACAGCACTTAATTA 1317
Db 961 GCTTCTGAAATCTTGCAATGTCATGTTGCTGCAATGAGTGCCTGACAGCACTTAATTA 1020

QY 1318 TTGCTTCAATTTGCGCGCATTTATGCTGTGTGGCTTCAACGAGGCGCTTGCAGTGGG 1377
Db 1021 TTGCTTCAATTTGCGCGCATTTATGCTGTGTGGCTTCAACGAGGCGCTTGCAGTGGG 1080

QY 1378 TTGTTACGCGAGAGTGTCTGCGGTGATTTGCGGAGCTTACGCTGATGAGTGTGTC 1437
Db 1081 TTGTTACGCGAGAGTGTCTGCGGTGATTTGCGGAGCTTACGCTGATGAGTGTGTC 1140

QY 1438 GTTTTATTAACCTTGTGTTTATTAATTAAGCCCGCTCTGCGCGCTGCGATGCTGCAC 1497
Db 1141 GTTTTATTAACCTTGTGTTTATTAATTAAGCCCGCTCTGCGCGCTGCGATGCTGCAC 1200

QY 1498 AGCAAGTTGTTCACTGTGTGTTGCTTGGCGTGATTTCTGATTCACCGTGAATGT 1557
Db 1201 AGCAAGTTGTTCACTGTGTGTTGCTTGGCGTGATTTCTGATTCACCGTGAATGT 1260

QY 1558 GCGCATGCGCGCATCACCAATGCTTCAGAGTCTAGCAATTTACCGCGAAATGTAGC 1617
Db 1261 GCGCATGCGCGCATCACCAATGCTTCAGAGTCTAGCAATTTACCGCGAAATGTAGC 1320

QY 1618 CACCTTGAATGATCAAACTCATGAGTTTCAACAACTTGGGTTGCTTGGCGCACTGC 1677
Db 1321 CACCTTGAATGATCAAACTCATGAGTTTCAACAACTTGGGTTGCTTGGCGCACTGC 1380

QY 1678 TTCAATCACTGCGCGTGGGTTTGGGTAGTGAATTTGCCGAGGCTAGTGTGC 1737
Db 1381 TTCAATCACTGCGCGTGGGTTTGGGTAGTGAATTTGCCGAGGCTAGTGTGC 1440

QY 1738 ACCAGCTTCAACCCATACCGTCAATTTCAGAGGGAATGAGTTTCTTCCAGAGGA 1797
Db 1441 ACCAGCTTCAACCCATACCGTCAATTTCAGAGGGAATGAGTTTCTTCCAGAGGA 1500

QY 1798 AGCTGACAGATTCAGCGCGCGAGAGAAAGCTCCAAAGCAATTAATCAAGATTGCGTAA 1857
Db 1501 AGCTGACAGATTCAGCGCGCGAGAGAAAGCTCCAAAGCAATTAATCAAGATTGCGTAA 1560

QY 1858 TAAAGGTAAATAATCAACTGCTTAAAGCGT 1887

Mon Aug 2 07:51:39 2004

us-09-963-521-1.rnpb

Page 21

Db 1561 TAAAGGTAAATCACTGCTAGGCGT 1590

Search completed: July 31, 2004, 10:01:29
Job time : 1227.59 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 31, 2004, 04:46:58 ; Search time 39 Seconds

(without alignments)
647.310 Million cell updates/sec

Title: US-09-963-521-2

Perfect score: 2432

Sequence: 1 MLSFATLRGRISTVDAAKAA.....QNGPRKRPXTNQRFGNKR 489

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCUS COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2432	100.0	489	US-09-431-099-2	Sequence 2, Appli
2	2432	100.0	489	US-09-431-099-4	Sequence 4, Appli
3	143.5	5.9	631	US-09-107-532A-3902	Sequence 3902, Ap
4	143	5.8	254	US-09-134-001C-5543	Sequence 5543, Ap
5	140.5	5.6	526	US-09-252-991A-23462	Sequence 23462, A
6	137	5.6	251	US-09-252-991A-22677	Sequence 22677, A
7	135.5	5.5	274	US-09-328-352-6673	Sequence 6673, Ap
8	134	5.4	274	US-09-134-001C-5279	Sequence 5279, Ap
9	132	5.4	657	US-09-252-991A-27682	Sequence 27682, A
10	129.5	5.3	424	US-09-543-681A-4762	Sequence 4762, Ap
11	128.5	5.3	304	US-09-540-236-3387	Sequence 3387, Ap
12	127.5	5.2	509	US-09-252-991A-32576	Sequence 32576, A
13	127	5.2	704	US-09-252-991A-30631	Sequence 30631, A
14	126.5	5.2	434	US-09-328-352-5070	Sequence 5070, Ap
15	126	5.2	734	US-09-252-991A-33036	Sequence 33036, A
16	125	5.1	638	US-09-252-991A-13036	Sequence 13036, A
17	125	5.1	977	US-09-134-000C-5653	Sequence 5653, Ap
18	124.5	5.1	525	US-09-107-532A-5743	Sequence 5743, Ap
19	124	5.1	474	US-09-489-039A-10432	Sequence 10432, A
20	124	5.1	569	US-09-252-991A-27248	Sequence 27248, A
21	124	5.1	996	US-09-252-991A-27018	Sequence 27018, A
22	123.5	5.1	242	US-09-107-532A-6251	Sequence 6251, Ap
23	123.5	5.1	421	US-09-489-039A-7699	Sequence 7699, Ap
24	123.5	5.1	515	US-09-252-991A-18662	Sequence 18662, A
25	123	5.1	459	US-09-134-000C-5404	Sequence 5404, Ap
26	123	5.1	477	US-09-489-039A-10570	Sequence 10570, A
27	122	5.0	468	US-09-252-991A-27966	Sequence 27966, A

28	121.5	5.0	356	4	US-09-134-000C-4914	Sequence 4914, Ap
29	121.5	5.0	410	4	US-09-328-352-4860	Sequence 4860, Ap
30	121.5	5.0	772	4	US-09-252-991A-30446	Sequence 30446, A
31	120.5	5.0	259	4	US-09-134-000C-6804	Sequence 6804, Ap
32	120.5	5.0	419	4	US-09-252-991A-23245	Sequence 23245, A
33	120.5	5.0	458	4	US-09-328-352-5083	Sequence 5083, Ap
34	120.5	5.0	500	4	US-09-252-991A-25053	Sequence 25053, A
35	120	4.9	444	4	US-09-328-352-6744	Sequence 6744, Ap
36	119.5	4.9	391	4	US-09-489-039A-9791	Sequence 9791, Ap
37	119.5	4.9	443	4	US-09-540-236-3307	Sequence 3307, Ap
38	119	4.9	473	4	US-09-489-039A-14022	Sequence 14022, A
39	119	4.9	494	4	US-09-328-352-7016	Sequence 7016, Ap
40	118.5	4.9	5588	3	US-09-036-987A-6	Sequence 6, Appli
41	118.5	4.9	5588	3	US-09-370-700-6	Sequence 6, Appli
42	118.5	4.9	5588	3	US-09-603-207-6	Sequence 6, Appli
43	118	4.9	438	4	US-09-540-236-2045	Sequence 2045, Ap
44	118	4.9	510	4	US-09-252-991A-29467	Sequence 29467, A
45	118	4.9	1241	4	US-08-714-741-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1									
US-09-431-099-2									
; Sequence 2, Application US/09431099									
; Patent No. 6410705									
; GENERAL INFORMATION:									
; APPLICANT: Degussa-Höls AG									
; TITLE OF INVENTION: New nucleotide sequences coding for the thre gene and process for									
; FILE REFERENCE: 990079 BT									
; CURRENT FILING DATE: 1999-11-01									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: Patentin Ver. 2.1									
; SEQ ID NO 2									
; LENGTH: 489									
; TYPE: PRT									
; ORGANISM: Corynebacterium glutamicum ATCC14752									
US-09-431-099-2									
Query Match									
Best Local Similarity 100.0%; Score 2432; DB 4; Length 489;									
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MLSFATLRGRISTVDAAKAA	PPSPPLAPDLDTHSGVAGVMTAARIGDILSSGTSNSD	60					
DB	1	MLSFATLRGRISTVDAAKAA	PPSPPLAPDLDTHSGVAGVMTAARIGDILSSGTSNSD	60					
QY	61	TKQVRAVTSAYGLYTHVDITNTTIFTNIGVERKMPNVHVHVGKIDTNSKISEVD	120						
DB	61	TKQVRAVTSAYGLYTHVDITNTTIFTNIGVERKMPNVHVHVGKIDTNSKISEVD	120						
QY	121	RLIRSIQAGATPEVEAKTIDELQSPASVGFVALLGMMMGAAVAVLLGGGQVSLTA	180						
DB	121	RLIRSIQAGATPEVEAKTIDELQSPASVGFVALLGMMMGAAVAVLLGGGQVSLTA	180						
QY	181	FTTAFITITATSTGLKKGIPTFQNVVGGFIATLPASIAVSALQGLBKPSQIIASGI	240						
DB	181	FTTAFITITATSTGLKKGIPTFQNVVGGFIATLPASIAVSALQGLBKPSQIIASGI	240						
QY	241	VLLAGLTIVOSQODGITGAPVTASARFPETILFTGIVAVGAGIQLSFIHVMIPAME	300						
DB	241	VLLAGLTIVOSQODGITGAPVTASARFPETILFTGIVAVGAGIQLSFIHVMIPAME	300						
QY	301	SAAPVYSSTFARIIAGGVTAFAVGVCAEWSVLIAGITLMSGAFYLLFVYLGPSV	360						
DB	301	SAAPVYSSTFARIIAGGVTAFAVGVCAEWSVLIAGITLMSGAFYLLFVYLGPSV	360						
QY	361	AAAIATATAGFGGILARFELPLIVATAGITPMIPGAIATRGVATINDGTIMGFNTI	420						
DB	361	AAAIATATAGFGGILARFELPLIVATAGITPMIPGAIATRGVATINDGTIMGFNTI	420						

Db 361 AAAAATAVGTGGTLARRFLIPLIYVAGITPMLGALAYRCMYATLNDQTMGEFTNI 420
 Oy 421 AVALATASSIAGVVLGEMWIRLRPRPNYPRAFTKANEFSFOEAEQNRQRKRPK 480
 Db 421 AVALATASSIAGVVLGEMWIRLRPRPNYPRAFTKANEFSFOEAEQNRQRKRPK 480
 Oy 481 TMOFRGNKR 489
 Db 481 TMOFRGNKR 489

RESULT 2

US-09-431-099-4
 ; Sequence 4, Application US/09431099
 ; Patent No. 6410705
 ; GENERAL INFORMATION:
 ; APPLICANT: Degussa-Höls AG
 ; APPLICANT: Forschungszentrum-Jülich GmbH
 ; TITLE OF INVENTION: New nucleotide sequences coding for the thr gene and process fo
 ; TITLE OF INVENTION: enzymatic production of L-threonine with corynebacterium bacteria.
 ; FILE REFERENCE: 990079 BT
 ; CURRENT APPLICATION NUMBER: US/09/431.099
 ; CURRENT FILING DATE: 1999-11-01
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 489
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum ATCC13032
 US-09-431-099-4

Query Match 100.0%; Score 2432; DB 4; Length 489;
 Best Local Similarity 100.0%; Pred. No. 4.1e-222;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MLSPATLGRISTVAAKAAAPPSPAPIDLTDSQVAGVMMLARIGDILISGTSMSD 60
 Db 1 MLSPATLGRISTVAAKAAAPPSPAPIDLTDSQVAGVMMLARIGDILISGTSMSD 60
 Oy 61 TKQVRAVTSAGLYTHVDITLNTITFTNIGVRKMPVNVFHVYVKLDTNFSKLEVD 120
 Db 61 TKQVRAVTSAGLYTHVDITLNTITFTNIGVRKMPVNVFHVYVKLDTNFSKLEVD 120
 Oy 121 RLIRSIQAGATPPPEVAEKILDELQSPASVGFPAVALLGMAMGGAVALLLGGQGVSLIA 180
 Db 121 RLIRSIQAGATPPPEVAEKILDELQSPASVGFPAVALLGMAMGGAVALLLGGQGVSLIA 180
 Oy 181 FTATFTIATTSFLKKGLPFPFQNVVGGFIATLPASIVSIALQFGLTKPSQIIASGI 240
 Db 181 FTATFTIATTSFLKKGLPFPFQNVVGGFIATLPASIVSIALQFGLTKPSQIIASGI 240
 Oy 241 VVLLAGLTLVQSLQDQITGAPVTASARFETLLFTGGIYAGVGLGIQSEIILHVMLPAME 300
 Db 241 VVLLAGLTLVQSLQDQITGAPVTASARFETLLFTGGIYAGVGLGIQSEIILHVMLPAME 300
 Oy 301 SAAANYSSTERRIAGVTAAPAVGCAEWSSVILGLTALMSAEVYLLFVYVLGPPS 360
 Db 301 SAAANYSSTERRIAGVTAAPAVGCAEWSSVILGLTALMSAEVYLLFVYVLGPPS 360
 Oy 361 AAAAATAVGTGGTLARRFLIPLIYVAGITPMLGALAYRCMYATLNDQTMGEFTNI 420
 Db 361 AAAAATAVGTGGTLARRFLIPLIYVAGITPMLGALAYRCMYATLNDQTMGEFTNI 420
 Oy 421 AVALATASSIAGVVLGEMWIRLRPRPNYPRAFTKANEFSFOEAEQNRQRKRPK 480
 Db 421 AVALATASSIAGVVLGEMWIRLRPRPNYPRAFTKANEFSFOEAEQNRQRKRPK 480
 Oy 481 TMOFRGNKR 489
 Db 481 TMOFRGNKR 489

RESULT 3

US-09-107-532A-3902
 ; Sequence 3902, Application US/09107532A
 ; Patent No. 6583275
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 ; NUMBER OF SEQUENCES: 7310
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Walham
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02354
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-ROM ISO9660
 ; COMPUTER: PC
 ; OPERATING SYSTEM: <Unknown>
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/107,532A
 ; FILING DATE: 30-Jun-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/085,598
 ; FILING DATE: 14 May 1998
 ; APPLICATION NUMBER: 60/051571
 ; FILING DATE: July 2, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Arinello, Pamela Deneke
 ; REGISTRATION NUMBER: 40,489
 ; REFERENCE/DOCKET NUMBER: GTC-012
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781)893-8277
 ; TELEFAX: (781)893-8277
 ; INFORMATION FOR SEQ ID NO: 3902:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 631 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: YES
 ; ORIGINAL SOURCE:
 ; ORGANISM: Enterococcus faecium
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (B) LOCATION 1...631
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3902:
 ; US-09-107-532A-3902

Query Match 5.9%; Score 143.5; DB 4; Length 631;
 Best Local Similarity 22.2%; Pred. No. 6.9e-05;
 Matches 97; Conservative 66; Mismatches 160; Indels 113; Gaps 22;

Oy 92 IGVRRKMPVNVFHVYVKL-----DTNFSKLEVDRLIRSIQAGATPPPEVAEKILDE- 142
 Db 41 VCGEENVS-NVYHCATRLRFTLKDKKADKEVEQLEGVITVEAGMGQVAVGNAVNEV 99
 Oy 143 -----LEQSPAS-----YGFPAVALLGM-AMMGGAVALLLGGQGVSLIAFTYA 184
 Db 100 YDVLISKQMKLEDDASGKRGTEKKGLINSFTIMAAVFPATLGVLAGSLINGVLAICTS 159
 Oy 185 FTIATTSFLKKGLPFPFQNVVGGFIATLPASIVSIALQFGLTKPSQIIASGIIVLL 244
 Db 160 INLUTTES-----GYIILNAAADAFYFLPFLFVAVTAKKENTD---RFTAMVTAAL 210
 Oy 245 AGTLTVQSLQDQIT---GAPVTASARFETLLFTGGIYAGVGLGI---QSEIILH---- 293
 Db 211 VYPTIVSAVSDSITLRFGLMPVIL-ARYNSTYI--PALLAVWLSTYIEPKIRKSLSHSIR 267
 Oy 294 -----WLPAMESAAP--NYSSTERRIAGVTA-----AAFAVGCAEWS 333
 Db 268 NLTPFCITVWPVILLVVGPIADYAS--QIIAGYLAVNVNFSVLTGAVIGGF--WQ 322

```

QY 334 SVLIA-----GLAAMGSAFYVLEVVYLGVSAAAIATATVGTGGL-----ARFRLP 383
Db 323 VLVITGLHWGLVPVMNNISFYGRDITLGPACMTAAVAQAQAVLGVLKTKRKKKSLSLSS 382
QY 384 PLIVAIAGIT-EMLPGL-----AIYRGMTATLNDQTLMGFTINIAVALATA 427
Db 383 APTLALFGITEPAVYGVTLKYKRPFIYACICGALFGVAGAAGAG-----ALAVATR 434
QY 428 SSLAAGVULGE---NI 440
Db 435 SLSFPIYIGBGFVWL 450

RESULT 4
US-09-134-001C-5543
; Sequence 5543, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: LYTH Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5543
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5543

Query Match 5.9%; Score 143; DB 4; Length 254;
Best Local Similarity 22.3%; Pred. No. 2e-05;
Matches 58; Conservative 51; Mismatches 139; Indels 12; Gaps 3;

QY 29 IDLDHSOYAGVMNLAIRIGDILSSGTNSDPTKVQVRAVTSAYGLYTHVDITLNTITI 88
Db 6 ITIIDENVIDIVLAIAGR---ILLEAGATYRIEPTMNRIAHSYGIHDTSFVSTAIF 62
QY 89 FTNIGVERKMPNVNHVVGKLDTFNFSKLSSEVURLRSTOAGTTPREVAEKIDELQSPA 148
Db 63 SLNDRTSKL-----IRIRERTDLEKALNTLSRSKSLTKOLTIDEAKSELLQKRASL 117
QY 149 SYGPEVALLGNAMGGAVALVIGGMOVSLIAFIATFIATTSFLGKKGLPTFFQNVYG 208
Db 118 QYSFELNLIAAFVACGFELFMFGVASDAMIACLAGIAFLFSPFVQXIQIKFSEFA 177
QY 209 GFIALPMSIAYSLALQGLRKPSQITASGIVLLIAGLTIVQSLQDGTGAPVTASARF 268
Db 178 SAVVISIAAIFTKIGIAKNQDI---ITYASVMPVPGILITNAIRDLAGELLAGMSRG 233
QY 269 FETLLFTGIVAGVGIQL 288
Db 234 VEALTFALIGAVAILLL 253

RESULT 5
US-09-252-991A-23462
; Sequence 23462, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 10/7196,136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23462
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23462

Query Match      5.8%; Score 140.5; DB 4; Length 526;
Best Local Similarity 19.1%; Pred. No. 0.0001;
Matches 94; Conservative 78; Mismatches 169; Indels 151; Gaps 19;

QY 10 RISTVDAKAAAP-----PPSLAPIDLTHSOVAGVNLARIIGDILLSSGTSNS 59
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 63 RAGTLPCRCGCPPTRMNGVCRIDPPS-----TTIRRGPADAPGRPADHGSMSADSNYS 116
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 60 DTKYQVAATVSAVGLYYTHVDITLNTLTTFINIGVEKRMVNVNHHVVGKIDTNSKISEV 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 117 QQPVPLAKRSALALSVMLGLTFRSASMTG-----GTLGTGUS----- 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 120 DRLTRISQAGATPPEVAEKILDELEQSPASYGPEFALLGWAMMGAAVAVLLGGGWQVSLI 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 -----YDDP-----FLAVLGLNMLGLYALIGFARGTGLS 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 AFTATFTTITSTSLGKKGGLPTFRQNVVGGFIATLPAST--ANSLAQFGLKIPSOIIA 237
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 189 THLLAHYSVRQOGLLAALGVA--RRHRGRLVRRRRSDVRPKYPVAATGIDVNLTLIVS 245
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 SGIVVL-----IAGTLTWSLQDQITGAPVTASARPETLLTFGGIYAGVGLIGLQSEIL 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 246 GALTMLTVFEGFAGLTILLSAI--AVPAIVVLGYSVWLAVRDAAGLAA-----LQOV- 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 293 HWMLPAMESAAAPNYSSTFARIITAGVTAAAFVAGCAEM-----SSVILIAGLTALMGSA 347
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 296 -----TPSAPLSTALALVGVSPVSGITLADPVRGRSARATVAVCVIAFFLGNS 347
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 348 FYIYFVYVYLGPEVSAALAAVAVGFTGGLARRPLIPLYIYALIGITPMLPGAIYGMYA 407
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 348 LMTLFE--GAAAGAAVAGKSDI--SDVMIAGGLIIPILVVL-----GLNITW----- 387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 408 TLNDQTL-----MGFTNTLA-----VALATASSL-----AAG 433
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 388 TTNDNMLYASGLGFANITGSSRFLLMLNGLALGTALMLYNHFVGMVTLFLSAIPIPG 447
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 434 VVIGWETARRLR 445
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 448 VTIADYLSRRRR 459
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-09-252-991A-22677
; Sequence 22677, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22677
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22677

```

Query Match 5.6%; Score 137; DB 4; Length 251;

Best Local Similarity 22.7%; Pred. No. 7.2e-05;

Matches 68; Conservative 27; Mismatches 134; Indels 70; Gaps 7;

160 AMMGAAVAVLLGGMOVSLIAFTIATTSFLGKGLPTFFONVVGFIAT-LPASI 218

2 ALVGAAPLIPAGVAAEALEAAAGLVAAAGFAAGAVAGL-----VAAAGFAATGFAAGL 55

219 AYSIALQFGLKIKPSQIIASGIIVVLLAGLTLVOSLQDGTGAPVATASAFETLLFTGGI 278

56 AAGFAAG-----AAGLAAGFAAADPATGIAAGFAAGFAAGLAAGFAAAVFAAGL 105

279 VAGVGLGIGLSEILHWMIPAMESAAAPVSTPARIITAGVTAAPNGCAEMSSVILA 338

106 AVGPAATGFAAGLAAGFAAAVFAAGLAAGFATGFAAGFAAGFAAAVFAAGLAAGFAAGFAV 165

339 GLTLMGSAFYLLFVVLGVPSAAAIAATAVGFTGGLARRELLPPLIVAIAGITPMLDG 398

166 GLAAGFAAGFAAAV-----AAGLAAGFAAGFAAGLAAGFAAGFAAGFAAGFAAGFAAG 194

399 LAIRGMVATINDQTLMGFTNIAVALATASSLAAGVIGEMIAIRLRPPFPNPPRAFT 457

195 -----GFAATVFTAGLAAGFAAGLVAG--FAURLSRA--LPASFT 231

RESULT 7

US-09-328-352-6673

; Sequence 6673, Application US/09328352

; Patent No. 6562358

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 6673

; LENGTH: 470

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-6673

Query Match 5.6%; Score 135.5; DB 4; Length 470;

Best Local Similarity 21.3%; Pred. No. 0.00026;

Matches 93; Conservative 51; Mismatches 141; Indels 151; Gaps 20;

89 FTNIGVERKMPVNVHVGKLDITNFSKLEVDRLIRSIQAGATPEVAEKIIDELEQSPA 148

119 FTFIGAPAKGP-----TEFAIL-----RFTAGLGIGVMMNVVALMTEVAPKIR 163

149 SYGFEVALLGMAMMGAAVAVLLG-----GMQVSLIAFTIATTSFLGKGLPTF 202

164 STLVAIMFSGYA-IGMTSALLGAWLVKDMGQ-----IMELLA-----GIPDL 206

203 FQNVVGFIATLPASIAVSIALQFGLKIKPSQIIASGIIVVLLAGLTIWOS-----LDDG 256

207 LIPILWKF--IPESLAFIVKSNHSEQ-----AKGIVSKIAPELTQANANTQVLNVEST 256

257 ITGAPVTA--SARFETLLF----- 274

257 TTDAVVRALFOQGRFSTFMFIAPMCLIMVYALGSMVPRKMLQAGVSLGSMFLFLPA 316

275 -TGGIVAGVGLG-----IQLSEILHWMIPAMESAAAPVSTPARIITAGVTAAPNGCAEMSSVILA 328

317 NIGGVGAIGGALADRFLIKPEVITIMF-IVGSA-----LILGINSPOFIL-- 363

329 YAEWSVLIAGLTALMGSAFYLLFVVLGVPSAAAIAATAVGFTGGLARRELLPPLIYA 388

364 --YSLINAGATIGSQILLYTTEVAQFP--TALRSGMAGAGI-----GRIGA 409

389 IAGITPMLPGIATIRGMVATINDQTLMGF-----TNIAVALATASSLAAGVIGEMIAIR 442

DB 410 IIG--PVLTG-----TLISFELPHQMNFLAIPGVIAALAFMVNLKASV 453

QY 443 ELRRPPFPNPPRAFTK 458

DB 454 AAOPTSTFNPNQTLTQ 469

RESULT 8

US-09-134-001C-5279

; Sequence 5279, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 5279

; LENGTH: 274

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-5279

Query Match 5.5%; Score 134; DB 4; Length 274;

Best Local Similarity 22.8%; Pred. No. 0.00016;

Matches 60; Conservative 50; Mismatches 123; Indels 30; Gaps 8;

29 IDLDHSCVAGVMMNLAANGILLSSGTSNSDITKVQVAVTSVAGLYTHYDITNTITI 88

26 IETSRALIKDVWIAAR---ILLESQAGETRVEDTARIAIKLGYPESNFPVT-NTVIE 81

89 FT--NIGVERKMPVNVHVGKLDITNFSKLEVDRLIRSIQAGATPEVAEKIIDELEQSPA 146

82 FVLNENAPR-----LYRITRDTNLIKISQANEISQIINGMTLEAKYQLEIYVA 135

147 PASYGFPVALLGMAMMGAAVAVL-----LGGWQVSLIAFTIATTSFLGKGL 199

136 KRDSLP-----FKGIAAIAIATSFVLYOGGRVLDITITFAGLTIYLVVEILDRKILH 188

200 PTFQNVVGFIATLPASIAVSIALQFGLKIKPSQIIASGIIVVLLAGLTIWOSLQDGTG 259

189 AOFIDFEGISLVIGIISVIGAFVPSGL-----ATIIAAVPIVPGVILTNALQDLRGG 244

260 APVTASARFETLLFTGIVAGV 282

DB 245 HMIPTTKSLBALVTARFAGIGAV 267

RESULT 9

US-09-252-991A-27682

; Sequence 27682, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196,136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 27682

; LENGTH: 657

; TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27682

Query Match 5.4%; Score 132; DB 4; Length 657;
Best Local Similarity 22.4%; Pred. No. 0.00091;
Matches 101; Conservative 67; Mismatches 157; Indels 126; Gaps 25;

```

QY 86 ITFTNGVERKMP---VNVFHVVGKLDTN-----FSKL-----SEVDRL 122
DB 110 VSIFS-----ROLPEVMARVLAVMGIMISGFEFLFIITTSNPFSLRLPQTRMODDNNLL 164
QY 123 IRSIQAGATPP-----EVAEKIDELQSPASYSYFPPALLGMAMGGA 167
DB 165 LQDGLIVHPPEMLYMGVGSVAFAPALAAVLGRLAAMARWSRPWTMAAFGLG--IG 222
QY 168 VLLG-----GWM-----QVSLIAFTFTFTIATTSFGKGLPFPQNVVGGF 210
DB 223 IVLGSMWVAYHELGMGWMFMDPVENASFPMLVGTALIHSLAVEKGV--FIS----- 274
QY 211 IATLPASIVASLALQFGLKPSQIIAS-----GIIVLLAGLTLV-QSLQDQITG 259
DB 275 WTVLIAIAAFSLSL-LGTFIVRSGLTSHVAHAFASDPERGVIILAFLLLVGGSLTLPALR 333
QY 260 APVTSARFF-----ETLFTGGIYAGVG-----LGQSEILHVMIPAMESAARPYSS 309
DB 334 APVKSQVGPALMSRETELLINLVVAASMLLGLTYPLLDLISGAKLSVGPPEFA 393
QY 310 TPARIIAGVTAFAFAVCAEMSSVLIAGITALMSGAFYLLFVYLGVPYSAALIAATAV 369
DB 394 MELELMA--ALMALAVGVLVRWKDTPSRMLGM-----LTPVLVASAVLAAA 439
QY 370 G-----FTGGLIARRELPPLIYVLAGITPMLPGAIYRGWATINDQTL---MGFTN 419
DB 440 GSWYFGDFENNAVLA-VELLSAMVY-LAGFRDFLDKTR-HKGVLAGASLIFRSYWGQLAH 496
QY 420 IAVALATASLAGVVL-GEMIAAR-LRRPP 448
DB 497 LGIAVC-----AIGIVLSQYSACRDLRMP 522

```

RESULT 10

US-09-543-681A-4762
Sequence 4762, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4762
LENGTH: 424
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-4762

Query Match 5.3%; Score 129.5; DB 4; Length 424;
Best Local Similarity 20.9%; Pred. No. 0.00081;
Matches 75; Conservative 40; Mismatches 116; Indels 127; Gaps 13;

```

QY 184 AFTIIATTSFLGKGLPTF-----FQNVGGFIIITLPASTIAYSLALQFGEIKRSQI 235
DB 40 ALIKIVTVSFF-WGLATITFALIVQPIILPKSESVTPATISLALSTGL----- 91
QY 236 IASGIVVLLAGLTLVSLQDGTGAPVTASARF--ETLL-----FTGGIYAGVGLGT 286
DB 92 -----MACGLIITGPLSDAFGRKNVIALFCAPFTIILSAMMNSMTGILITRALVGL 144
QY 287 QLSLILHVMIPAMESAARPY-----SSTFARIAGVTAFAFAVCAEM 332

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DB 145 SLSGVAANVMTYISEIHPAYIALSMGLYISGNSIGMSGRVITG-----VLSDYYSW 197

QY 333 S-SVIITGLTALMGSAFY-----LFF----- 353

DB 198 RVSIIILGIFALVAAILFWKILPFSQHFPAITLKPRNLITTKLHFEDKGLPLFLFIGGL 257

QY 354 -----VYLGVSAAAIATAVGTGGLIARRELPPLIYA 388

DB 258 IMGGFVTLFNYIGRLIDAPYSILQTVGLISYLSGTYASAKAGLLTNKYGK--VF 315

QY 389 IAGTPELPGIATYRCGYATINDQTMGFNIAVALTASGLAAGVVLGEMTARLR 446
DB 316 IAGVSMILAGILIL-----TLFDSLAIIF--IGMLIITGTFPAHAHAASSWGRARR 365

RESULT 11

US-09-540-236-3387
Sequence 3387, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATALA
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540.236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3387
LENGTH: 304
TYPE: PRT
ORGANISM: M. catathalis
US-09-540-236-3387

Query Match 5.3%; Score 128.5; DB 4; Length 304;
Best Local Similarity 18.7%; Pred. No. 0.00061;
Matches 60; Conservative 60; Mismatches 134; Indels 67; Gaps 8;

```

QY 13 TVDAAKAAPPPSELPAPIDLD-----HSQVAGVNNIARIGDILSSGTS 57
DB 8 TIQATKSHF-----MNLADDEMPSLFDPHPSRLNAAQQRITRLICRCLLIMQGA 61
QY 58 NSDPTKQVRAVTSAYGLYTHVDITNTITFT-----NIGVERMPYVNF 103
DB 62 SVVVVDLTKRLGALGIDGVEGSLFNAVTLTLYQRCITTYRNVTHQGINVSLVQIQ 121
QY 104 HVGXKJDTNYSKISEV-----DLRISIQAGATPREVAEKIDELQSP-----ASYGF 152
DB 122 QILISAHENHOANOSHCLINTOSHDACTSSVQG-----PDATYQTVYSNHLVSFPV 171
QY 153 PVALLGMAMMGAAVAVLLGGWQVSLIAFTFTIATTSFLGKGLPFPQNVVGGFIA 212
DB 172 GVCASFAVANGATIV-----IALITFASIVAMLRVYLKQHNPPVVMITAFYA 224
QY 213 TLPASTIAYSLALQFGEIKRSQIIASGIVVLLAGLTVSLQDGTGAPVTASARFETL 272
DB 225 TLIAALAYFNLGTNADI-----AVASVLLHVSFPPIINALSLIKGYMMNGVRMFPAT 280
QY 273 LFTGGIYAGVGLGQSEILH 293
DB 281 MLTISACVGIWTLIFLRIPH 301

```

RESULT 12

US-09-252-991A-32576
Sequence 32576, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A

```

: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ. ID NOS: 33142
: SEQ. ID NO 32576
: LENGTH: 509
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32576

```

Query Match	5.2%;	Score 127.5;	DB 4;	Length 509;
Best Local Similarity	26.7%;	Pred. No. 0.0017;		
Matches 70;	Conservative 31;	Mismatches 88;	Indels 73;	Gaps 13;

```

QY      236  IASGI VLLIAGLITVLSIDGGITGAPVVA---SARFFETLLFTGTGIVAGVGLIGQLSEIL 292
      255  LAAGVAAAGAG-----ALEDAAGAGPAAAGLAAGFFAAGFFAAGLAAGPAG----- 302
DQ      223  HVM LPMESA--AAPNYSSTPARIITAGVT---AAAPVCGIAEMSVYIAGLTALMGSA 347
      303  ---LAAVAAAGLAAGAPFAAFAAALAGLVAGFAAAPVGLAAG---LAAGGLAAVFAA 355
DQ      348  FYLLFVVIYIGPVSAALIAATAVGTGGLIARFLLPLIVAIAGITPMLPGIATYRGMYA 407
      356  GF-----FAAGPAGAGLAALILAGLAAGLAAYF-----AGGLA--AGFAA 393
DQ      408  TLNDQTLMGFT---NIAVALATASSLAAGVVLGEMIRLRRLRPPR-FNPYRAFTKANEF 462
      394  GLAAAPAGLITLPVPSFICIVSVSTL---LCSFSTSLRGTGPRREMLFRRISKASS 449
DQ      463  S-----FOREAE 469
      450  SLHLPPARSRTSLTIFAERAE 471
DQ

```

RESULT 13
US-09-252-991A-30631
; Sequence 30631, Application US/09252991A

```

1  GENERAL INFORMATION:
2  APPLICANT: Marc J. Rubenfield et al.
3  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
4  TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
5  FILE REFERENCE: 107196.136
6  CURRENT APPLICATION NUMBER: US/09/252,991A
7  CURRENT FILING DATE: 1999-02-18
8  PRIOR APPLICATION NUMBER: US 60/074,788
9  PRIOR FILING DATE: 1998-02-18
10 PRIOR APPLICATION NUMBER: US 60/094,190
11 PRIOR FILING DATE: 1998-07-27
12 NUMBER OF SEQ ID NOS: 33142
13 SEQ ID NO 30631
14 LENGTH: 704
15 TYPE: PR1
16 ORGANISM: Pseudomonas aeruginosa
17 US-09-252-991A-30631

```

Query Match	127;	Score	5.28;	DB	4;	Length	704;
Best Local Similarity	22.18;	Pred.	No. 0.003;				
Matches 102; Conservative	63;	Mismatches	156;	Indels	140;	Gaps	24

```
QY      44 AARGDILLSSGNSDSNDRKQVRAVL-----SARGLV-----YTHVDITLNTITFINIG   93
Db      37 AAALGYVALLRGAIALNALMIVAAVAIYVAIRYSPLPSAKWMDLDNRKATPRAYLANNDG   96
QY      94 VERKPMVNPFHVVGKLDITFNSKLSSEVDRLIRSIOGARP-----PEVAEKILDELSOSPASY 156
Db      97 LD-YVFNNKHILFGH---HPAAL-----AGAGLVGPVLA-----ACM 130
QY      151 GEFVALLGNMMMGAVALLGGGWQVSLAFITA----- 184
```

Dh 133 GYLPGTL-WLNG-----VVLGAVQDDPFWVLISRRNGRSIGELVREMQVAGTIALFCG 185

Qy 185 -----FTIATSTSELRKGLPFPPQNVVGF--IATPASTATSLAQFGLEIKP---SQ 234

Dh 186 AFLIMITIIATLIALIVTALA--DSPGMVTATATPTIALEMGVNFR---IRPGIGE 239

Qy 235 IASGIIVVLIAGLTIVOSLODGIITGAPATASAREFETLLFTGTIVAG--VGLGIOLSEIL 292

Dh 240 ISIIIGVETLLSIGWL-----GGVPAAPSEWAPHTFEGSIQITWMLIGYCAVAS--- 287

Qy 293 HWVLPMESAAPNPVNSTPARIINAGVYAAAFVAGCAEWSVLIAGLTTL-----M 344

Dh 288 --VLPFWILLARPDYSLFKI---GTTGLAIGILIVPELMKPLDTPFTDGTGVWK 341

Qy 345 GSAFYVLFW-VYLGPVSA--PAIA-----ATAVGFTGILLARFLLPPIVA 388

Dh 342 GSIFFPLFTIICGAWSGCFHALISSGTPKLLINREPDARIYG--GGMIMESFVAIMAMVA 400

Qy 389 IAGITPMLPGAIYRGMYATLNDQILMFGTIIAVALTASS 429

Dh 401 ASVIEP-----GIYFAMMSPPAVVGADVAMVAALVSS 432

```

RESULT 14
US-09-328-352-5070
; Sequence 5070, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5070
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5070

```

Query Match	5.2%	Score 126.5	DB 4	Length 434
Best Local Similarity	22.8%	Pred. No. 0.0016		
Matches 89	Conservative 50	Mismatches 161	Indels 91	Gaps 19

```

QY      118 EYVRLIRLSIQAGTTPREVEAKILDEEOSPASVGPV---ALLG-----AMMGAAVAV- 168
Db      17 DVCH--RPVSTMEYLPVQSAILG-IQAFAFMFGATVLAPLMGFNPMIALMSGICTIL 73
QY      169 --LGGGWOVSLIAFITAF--TIIATSPFLKCKGLPTEFQNVGGFATLPASIAYSIAL 224
Db      74 FLITGGRPVSYLGSSEFAFIGVAATAGHTTSGGANPMIALGIVA---CGIFVAL-- 128
QY      225 QFGELET-----KPSQIIASGIVALLAGTLTVQSIQDGIITAP----- 265
Db      129 -IGFIWLTGTRNIEKMLMPVVTGAIWMTIGINTLPVTIKVACQPFEMMALITVLQMG 187
QY      262 ---VTASARFETFLPTGGIVA-----GVGLG--IOLSEIHLWMLPAMESAAAPNY 307
Db      188 STAVFRGELLQRLILLVGLILAVIYATATNGLGIGRKIDPSQILQASWFOIPEFSHPTE 247
QY      308 SSTFARIIA-----GGVTAAPAAVAGCYAEMSSVITAGLTALMGSAFY--LFTV 355
Db      248 DTKAILIIPVALIIVAEMLGHIKAVGAMTG-----ENLTPQKGAFFVADGLATT 297
QY      355 YLGPVSAALIAATAVGFTGGLARRFLPPLILVAIAGITPMLPGIA-IYRGMVATINDQT 411
Db      298 LSGSVGAPGM--TTYGENIGVMAVTVRVYSTIVFVINGAIFALFLGSPKFGAVISTPBSAV 355
QY      414 LMGFTNIAVALATPASSLAAGVVLGEMTARLL 444
Db      356 LTGASIVVFGILT---IAGAKI--WIENKU 380

```

RESULT 15

US-09-252-991A-33036

Sequence 33036, Application US/09252991A

Patent No. 6551795

; GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196 136

CURRENT APPLICATION NUMBER: 10/136.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 33036

; LENGTH: 734

TYPE: PRT

ORGANISM:

US-09-252-991A-33036

Quinn-Kearney

Query Match	Score	DB 4	Length
5.28	126	734	

Best Local Similarity 21.9%; Pred. No. 0.004;

Matches 126; Conservative 60; Mismatches 184; Indels 206; Gaps 26;

QY 18 KAPPPSPAPIDLTDSQVGV-----MNLARIGDILLSSGTS-----NSDTKVQV--- 65

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LS / KQAEFHSFEE-SLVERGFMAAKGMLFGGNI.VLRIGVLLFGLAFLTRYASERVAAPVE 215

66 -----PAYTSAYGTYTHDITNTTETENNICYEBKBYNUEWY 10E

[illegible]

Db 216 YRYAGVALAAMALLGVGWWLRERRAAYGLLQGTGIAVLVLTIFAAM----- 262

106 VGKLDTNESKLSKVDRILRSIOAGA-----TPPEVAEKTI,DEL,EOSPASVGEPPVAT,IGWA 160

NAME	DATE	TIME	LOCATION	REMARKS
JOHN DOE	10/10/2023	14:30	Room 101	Completed task
JANE SMITH	10/10/2023	15:00	Room 102	Meeting with client
...

263 -----RLHPLISPGALALLVVMICSAIILVQNA-----MGLAVVA 300

161 MMGGAYVAVIT.L.-GCCGNOVSTTAFTHFM-TTATTCCTCVCATDDETCVTHNCAHTTATDCTC

[illegible]

Db 301 ALGGFAPIITSTGSGNHVALFSYFALLNAGIFAIAFWRAWRP L-----NLV-GFVGT-- 352

216 ASIAYSLAOFGLKPSOTIAS-----GTWTLAGITLMSI.D-GTTGAP 261

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Search completed: July 31, 2004, 10:02:10
Job time : 42 secs

Job time : 42 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 31, 2004, 10:01:43 ; Search time 110 Seconds
(without alignments)
2467.009 Million cell updates/sec

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Perfect score: 2432
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Ygapop 10.0 , Ygapext 0.5
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2432	100.0	1909	US-09-431-099-3	Sequence 3, Appli
2	2432	100.0	2817	US-09-431-099-1	Sequence 1, Appli
3	591	24.3	4403765	US-09-103-840A-2	Sequence 2, Appli
4	591	24.3	4411529	US-09-103-840A-1	Sequence 1, Appli
5	190	7.8	9834	US-08-956-171E-37	Sequence 37, Appl
6	169.5	7.0	18436	US-08-961-527-87	Sequence 17, Appl
7	165	6.8	23210	US-09-596-003-17	Sequence 17, Appl
8	146.5	6.0	912	US-09-252-991A-6186	Sequence 6186, Ap
9	146.5	6.0	913	US-09-252-991A-6445	Sequence 6445, Ap
10	146.5	6.0	1806	US-09-252-991A-6023	Sequence 6023, Ap
11	143.5	5.9	1896	US-09-107-531A-248	Sequence 248, App
12	143	5.9	765	US-09-134-001C-2706	Sequence 2706, Ap

13	142.5	5.9	1581	4	US-09-252-991A-7755	Sequence 7755, Ap
14	140.5	5.8	1581	4	US-09-252-991A-6891	Sequence 6891, Ap
15	140.5	5.8	1941	4	US-09-252-991A-6778	Sequence 6728, Ap
16	138.5	5.7	1200	4	US-09-252-991A-6282	Sequence 6282, Ap
17	137	5.6	756	4	US-09-252-991A-6106	Sequence 6106, Ap
18	137	5.6	4881	4	US-09-252-991A-7234	Sequence 7234, Ap
19	137	5.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
20	135.5	5.6	1413	3	US-09-328-352-2547	Sequence 2547, Ap
21	135	5.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
22	134	5.5	825	4	US-09-134-001C-2442	Sequence 2442, Ap
23	132	5.4	1974	4	US-09-252-991A-1111	Sequence 1111, A
24	129.5	5.3	1275	4	US-09-543-681A-590	Sequence 590, App
25	129.5	5.3	12127	4	US-08-961-527-148	Sequence 148, App
26	128.5	5.3	915	4	US-09-540-236-1467	Sequence 1467, App
27	128.5	5.3	1683	4	US-09-252-991A-11226	Sequence 11226, A
28	128.5	5.3	2085	4	US-09-252-991A-14016	Sequence 14016, A
29	128.5	5.3	2115	4	US-09-252-991A-14060	Sequence 14060, A
30	128.5	5.3	2397	4	US-09-252-991A-14210	Sequence 14210, A
31	128.5	5.3	3087	4	US-09-221-017B-81	Sequence 81, Appl
32	128	5.3	2217	4	US-09-252-991A-10720	Sequence 10720, A
33	128	5.3	2526	4	US-09-252-991A-10348	Sequence 10348, A
34	128	5.3	2921	4	US-09-252-991A-11395	Sequence 11395, A
35	127.5	5.2	951	4	US-09-252-991A-16386	Sequence 16386, A
36	127.5	5.2	1092	4	US-09-252-991A-16212	Sequence 16212, A
37	127.5	5.2	1530	4	US-09-252-991A-16005	Sequence 16005, A
38	127	5.2	10146	4	US-08-956-171E-243	Sequence 243, App
39	126.5	5.2	1305	4	US-09-328-352-944	Sequence 944, App
40	126.5	5.2	1503	4	US-09-252-991A-8482	Sequence 8482, App
41	126	5.2	1407	4	US-09-252-991A-11395	Sequence 11395, A
42	126	5.2	2205	4	US-09-252-991A-16465	Sequence 16465, A
43	126	5.2	2256	4	US-09-252-991A-16137	Sequence 16137, A
44	126	5.2	2871	4	US-09-252-991A-11431	Sequence 11431, A
45	126	5.2	38675	4	US-08-311-731A-135	Sequence 135, App

ALIGNMENTS

RESULT 1
US-09-431-099-3
Sequence 3, Application US/0941099
Patent No. 6410705
GENERAL INFORMATION:
APPLICANT: Degussa-Höls AG
TITLE OF INVENTION: Forschungszentrum Jülich GmbH
TITLE OF INVENTION: New nucleotide sequences coding for the thr gene and process for
CURRENT APPLICATION NUMBER: US/09/431,099
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1909
TYPE: DNA
ORGANISM: Corynebacterium glutamicum ATCC13032
FEATURE:
NAME/KEY: CDS
LOCATION: (280)..(1746)
OTHER INFORMATION: thrE-gen
US-09-431-099-3

Alignment Scores:

Pred. No.: 9.87e-264
Score: 2432.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Gaps: 0
US-09-963-521-2 (1-489) x US-09-431-099-3 (1-1909)

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 QY 21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
 Db 340 CCTCCGCCATCGCCATCAGCCCCGATGTGATTCACAGCACCATAGTCAAGTGGCCGATG 399
 QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
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 QY 61 ThrIlyValGlnValArgAlaValThrSerAlaThrGlyLeuThrTyrrThrsIlyValAsp 80
 Db 460 ACCAAGGTACAAATTCGAGCAGTGAAGCTTCGCGACGTTTGACTACACGACGAGAT 519
 QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgIlySmetProVal 100
 Db 520 ATCAGCGTGAATACGATCACCACATCTTCACCAACATGGTGGAGAGAAAGATGCCGCT 579
 QY 101 AsnValPheHisValValGlyLysLeuAspThrAsnPheseIySLeuSerGlyValAsp 120
 Db 580 AACGTGTTGATGTTGAGGCAAGTTGGACACCAACTTCTCCAAACTGCTGAGGTTGAC 639
 QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGlnValAlaGlnLysIleLeu 140
 Db 640 CGTTTGATCGGTTCCATTCAGGCTGGTGCAGACCCGCTGAGGTTGCCGAGAAATCTCTG 699
 QY 141 AspGlnLeuGlnGlnSerProAlaSerTyrrGlyPheProValAlaLeuLeuGlyTyrrAla 160
 Db 700 GACGAGTTGAGACATCCCTGGCTCTTAAGTTTCCCTGTTGGCTTGCTGGCTGGGCA 759
 QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyTyrrGlnValSerLeuIleAla 180
 Db 760 ATGATGGTGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 819
 QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysGlyLeuPro 200
 Db 820 TTTAATACCGGTTGACGATATTGTCACACGATCATTTTGGGAAAGAGGTTTGCT 879
 QY 201 ThrPhePheGlnAsnValAlaGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyrr 220
 Db 880 ACTTCTTCCAAAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAT 939
 QY 221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLysProSerGlnIleIleAlaSerGlyIle 240
 Db 940 TCTTGGCGTTGCAATGTGTGTGAGATCAACCGACCGACATCTGCAATTCGGAATT 999
 QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260
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 QY 341 ThrAlaLeuMetGlySerAlaPheTyrrLeuPheValAlaTyrrLeuGlyProValSer 360
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 QY 361 AlaAlaAlaIleAlaAlaThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgIlyPhe 380
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QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
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 QY 401 IleTyrrGlyMetTyrrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
 Db 1480 ATTTACCGCGGATGTACCGCACCTCGAATGATCAACATCACTAGGTTTACCAACATT 1539
 QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGlnTyrrPhe 440
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 Db 1660 GAGTTCTCTTCCAGAGGAGAACTGAGCAGATCAAGCGCGCAGAGAAACGTCGCAAG 1719
 QY 481 ThrAsnGlnArgPheGlyAsnIlySArg 489
 Db 1720 ACTAATCAGAGATTCGTTAATAAAAGG 1746

RESULT 2

US-09-431-099-1
 ; Sequence 1, Application US/09431099
 ; Patent No. 6410705
 ; GENERAL INFORMATION:
 ; APPLICANT: Degussa-Höls AG
 ; APPLICANT: Forschungszentrum-Joachim GmbH
 ; TITLE OF INVENTION: New nucleotide sequences coding for the thrE gene and process for
 ; TITLE OF INVENTION: enzymatic production of L-threonine with coryneform bacteria.
 ; FILE REFERENCE: 990079 BT
 ; CURRENT APPLICATION NUMBER: US/09/431, 099
 ; CURRENT FILING DATE: 1999-11-01
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2817
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum ATCC14752
 ; FEATURES:
 ; NAME/KEY: CDS
 ; LOCATION: (398)..(1664)
 ; OTHER INFORMATION: thrE-Gen
 US-09-431-099-1

Alignment Scores:

Pred. No.: 1,87e-263 Length: 2817
 Score: 2432.00 Matches: 489
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-963-521-2 (1-489) x US-09-431-099-1 (1-2817)

QY 1 MetLeuSerPheAlaThrLeuArgIlyArgIleSerThrValAspAlaIlyAlaAla 20
 Db 398 ATGTTGATTTTGGACCCCTTCGTGGCGCATTTTCMAAGTTGAGCTGCAGAAAGCCGCA 457
 QY 21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
 Db 458 CCTCCGCCATGCGACACTGAGCCCGCATTAATCTCACTGACCAATGACAGTGGCGGTG 517
 QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
 Db 518 ATGAAATTTGGCTGCGAGAAATTCGATATTGCTTTCTTCAAGTACGTCGCAAAACGTGAT 577
 QY 61 ThrIlyValGlnValArgAlaValThrSerAlaTyrrGlyLeuTyrrThrsIlyValAsp 80

Db 578 ACCAAGGTGCAAGTTCAGAGCGGTGACCTGCGTATGCGCTGTAATACCATGTGGAT 637
 QY 81 ILeThleuSsnThrlIethrIlePheThrsnIleGIyValGuaArgLysMetProVal 100
 Db 638 ATACCGTGAATGCATCCACCATCTTCCAAACATCGGTGGAGAGAAAGATCCGGCT 697
 QY 101 AsnValPheHisValValGlyLysLeuAspThrsnPhseSerLysLeuSerGluValAsp 120
 Db 698 AACGTGTTTCAATGTTGGGCAAGTTGACACCAACTTCTCCAAACGTCTGAGGTGAC 757
 QY 121 ArgLeuIleArgSerIleGlnIleGlyAlaThrProProGluValIleGlyLysIleLeu 140
 Db 758 CGTTTGATCCGTTCCATTCAGCGCTGCTGCTACCCCGCTGAGGTTGCCGGAATAATCTG 817
 QY 141 AspGluLeuGluGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrPala 160
 Db 818 GACGAGTTGAGCAATGCGCTGCGTCTTATGCTTCCCTGTTGCTTGGCTGGCGCA 877
 QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyGlyTyrPalaSerLeuIleAla 180
 Db 878 ATATGAGGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 937
 QY 181 PheIleThrsAlaPheThrlIleIleAlaThrThrsPheLeuGlyLysLysGlyLeuPro 200
 Db 938 TTTATTACCGCGTTCCAGATCATTCGACAGACGCTCATTTTGGAAAGAGGTTTGCT 997
 QY 201 ThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr 220
 Db 998 ACTTCTTCCAAATGTTGTTGTTGTTTATGTCACAGCTGCTGCATGATGCTT 1057
 QY 221 SerLeuAlaLeuGlnPheGlyLeuGluIleLysProSerGlnIleIleAlaSerGlyIle 240
 Db 1058 TCTTTGGCGTTGAATTTGCTTGAATCAACCAAGCAGCAATTCGATCGAAT 1117
 QY 241 ValValLeuLeuAlaGlyLeuThrlLeuValGlnSerLeuGlnAspGlyIleThrsGlyAla 260
 Db 1118 GTTGCTGCTTGGACGTTTGACATCTTGCAATCTCTGACAGACGCAATCACGGCGCT 1177
 QY 261 ProValThrsAlaSerAlaArgPhePheGluThrlLeuLeuPheThrsGlyIleValAla 280
 Db 1178 CCGGTGACAGCAAGTGCAGATTTTGAACACTCTGTTTACCGCGGCAATGTTGCT 1237
 QY 281 GlyValGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu 300
 Db 1238 GCGGTGGGTTTGGCAATTCAGCTTCTGAATCTTGCAATGTCATGTTGCTCCACGAGAG 1297
 QY 301 SerAlaAlaAlaProAsnTyrSerSerThrsPheAlaArgIleIleAlaGlyGlyValThr 320
 Db 1298 TCCGCTGACGACACTAATATTGCTGTAATTCGCGCCGCAATTCGCTGCGCTGAC 1357
 QY 321 AlaAlaAlaPheAlaValGlyCysTyrAlaGluTyrPheSerValIleIleAlaGlyLeu 340
 Db 1358 GAGAGGCGCTTGGAGTGGTGTGTAACGGAGTGTCTCCGTGATTAATTCGAGGCTT 1417
 QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProAlaSer 360
 Db 1418 ACTGCGCTGATGGGTTCTGCGTTTATTAACCTTCTGCTGTTATTAAGCCCCGCTCT 1477
 QY 361 AlaAlaAlaIleAlaAlaThrAlaValGlyPheThrsGlyGlyLeuLeuAlaArgPhe 380
 Db 1478 GCCCGTGCAGATTCGCAACAGCAGTGTGTTCACTGGGTGTTGCTTCCCGCTGATTC 1537
 QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
 Db 1538 TTGATTTCCACCGTTGATTTGGCGATTCGCGGACACACCAATCTTCCAGGTCTACCA 1597
 QY 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrlLeuMetGlyPheThrsnIle 420
 Db 1598 ATTTACCGCGAATTAACGACCTTGATGATCAACATCACTATGAGGTTTCAACCAACT 1657
 QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGluThrIle 440
 Db 1658 GCGGTGCTTAAAGCACTGCTTCACTTCGCGCTGCGTGGTGGTGGTGGTGGTGGT 1717

QY 441 AlaArgLeuAlaArgProProArgPheAsnProTyrArgAlaPheThrlValAsn 460
 Db 1718 GCCCGAGAGCTAGCTGCTCCACACCTTCAACCATACCTGATTTACCAAGCGAAT 1777
 QY 461 GluPheSerPheGlnGluGluAlaGluGlnAsnGlnArgArgGluArgLysArgProLys 480
 Db 1778 GAGTTCCTCTTCCAGAGGAGAACTGAGCAATCAAGCGCGCGGAGAGAAAAAGTCCAAAG 1837
 QY 481 ThrAsnGlnAlaArgPheGlyAsnLysArg 489
 Db 1838 ACTAATCAAGATTCGATATAAAGG 1864

RESULT 3

US-09-103-840A-2
 ; Sequence 2: Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

Alignment Scores:

Pred. No.: 7 1e-51 Length: 4403765
 Score: 591.00 Matches: 167
 Percent Similarity: 50.86% Conservative: 69
 Best Local Similarity: 35.99% Mismatches: 174
 Query Match: 24.30% Indels: 54
 DB: 3 Gaps: 12

US-09-963-521-2 (1-489) x US-09-103-840A-2 (1-4403765)

QY 7 LeuArgGlyArgIleSerThrsValAspAlaAlaValAlaProProSerProLeu 26
 Db 4179998 CTGCGCGGCGC-----CGGATCCGCTGCCGCG 4180027
 QY 27 AlaProIleAspLeuThrsPheHisSerGlnValAlaGly----- 39
 Db 4180028 GCG-----GCGCGGCGAGCCGCACTCGCGGAAATCGTGACCTGCACACC 4180075
 QY 40 -----ValMetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSer 57
 Db 4180076 CGGAAGTGTGACCTAACAATCGGCTCGCGGAGGATGTGTGCTCGGCTCGGC 4180135
 QY 58 AsnSerAspThrLysValGlnValAlaValThrsAlaTyrGlyLeuTyrTyrThr 77
 Db 4180136 ACCGCGATGTCGTGCACAGCCAGACGTCAGGCTACAGCTCACCGATTC 4180195
 QY 78 HisValAspIleThrlLeuAsnThrlIethrIlePheThrsnIleGlyValGluArgLys 97
 Db 4180196 GTTGTGCATCACCGCTTACCAACATC---ATCGGTCCGCGCTGACGACACACACT 4180252
 QY 98 MetProValAsnValPheHisValValGlyLysLeuAspThrsAsnPhseSerLysLeuSer 117
 Db 4180253 CCGCGGTACACCAATCAGCGGTGCGTCCGAGCCGGTCTCACTGACTACAGCGGCTGGCC 4180312

QY	118	GlulValAspArgLeuLeuLeuLeuSerIleGlnAlaGlyAlaThrProProGluValAlaGlu	137
Db	4180313	GAACCTCATGACACTGCTTCAACGGGAATPAACTCCGGTGGCGCTGCAGATCAACCAAGCTCAC	4180372
QY	138	LyelLeuAspGluLeuGluGlnInsSerProAlaSerTyrGlyPheProValAlaLeuLeu	157
Db	4180373	GAGGCTATGGACGAGTTTGACCGAAGCGGCCCAACCCCTAACCCGCGCTGGCTCGGACCGGG	4180432
QY	158	GlyTyrAlaMetMetGlyGlyAlaValAlaValLeuLeuGlyGlyGlyTyrPglValSer	177
Db	4180433	GGGGCGCGGGCTTCGACACTCGGCGTCCCATGTGCTCGGGCGGAACCTGGCTGACCTGG	4180492
QY	178	LeuIleAlaPheIlePheIlePheAlaPheThrIleIleAlaThrThrSerPheLeuGlyLys	197
Db	4180493	GTCCTGGCTGCCGCGACGCTCTGGGTATGACCGACCGATGGGCGCGGCTGTAACCGGATC	4180552
QY	198	GlyLeuProThrPhePheGlnAsnValAlaGlyGlyPheIleAlaThrLeuProAlaSer	217
Db	4180553	GGGACCCCGTGTGTCTTCCACGCGGTTCGGCGCGGGAGTCGGGAGCCCTGGTGGCGGTG	4180612
QY	218	IleAlaTyrSerLeuAlaLeuGlnPheGlyLeuGluTyrLeuLysProSerGlnIleIleAla	237
Db	4180613	CGCGCTTACCTCGATCGCCGGCCAG-----GATCCGACCGGGCGTGGTGGCC	4180657
QY	238	SerGlyIleValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIle	257
Db	4180658	ACCGGAATCGTTGTGCTGCTCTCTGGATGACCTTGTGGGTTTCGATGACGAGACCGCGTC	4180717
QY	258	ThrGlyAlaProValAlaThrAlaSerAlaIlePhePheGlnThrLeuLeuPheThrGly	277
Db	4180718	ACCGGGATCATGCTTCAACCGCACTCGCCCGGCTTGGCCACGCGCTTCTTCGACCGCAGGG	4180777
QY	278	IleValAlaGlyVal-----GlyLeuGlyIleGlnLeuSer	289
Db	4180778	ATCGCTCGTGGCATCTCATCTCGTTCGGGGCGGCTACCAATGCGGCATTCAGATGAA	4180837
QY	290	GluIleLeuHisValMetLeuProAlaMetGlnSerAlaAlaAlaProAsnTyrSerSer	309
Db	4180838	-----CTGCATGTC-----GAGCGAACCAACGACGCTCGCACCCCGGCGATCCGCTA	4180885
QY	310	ThrPheAlaArgIleIleAlaGly-----GlyValThrAlaAlaAlaPheAlaValGlyCys	328
Db	4180886	CCGATTCCTCGCGCGGTAAAGCGTGGCGGCTGTGTCGGCGGTGCTGACGATCGCAGAC	4180945
QY	329	TyrAlaGluTyrPheSerSerValIleIleAlaGlyLeuThrAla-----	342
Db	4180946	TATGGCGCGCTACGTTCTGTGGCCACCGCCGACACTCTGGCGGACCTGCCGAATCGGTG	4181005
QY	343	LeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProValSerAlaAla	362
Db	4181006	CTCATCGGA-----CTCGCGCGCGCGGGGTTCGCGCAGTGTGTGCGCAC	4181056
QY	363	AlaIleAlaAlaThrAlaValAlaGlyPheThrGlyGlyLeuAlaAlaArgArgPheLeuIle	382
Db	4181051	TGGACCGCGCGCATCGGCGTGGCTTCTTGGCACCTCATCTCATCTCATCGTGGCGAGCT	4181110
QY	383	ProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAlaIleTyr	402
Db	4181111	CCCGCTGTGTAAACGCCACCGCCGCGCATACCGGATGCTGCCGGGCTTGGCGGTCTTC	4181170
QY	403	ArgGlyMetTyrAla-----ThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIleAla	421
Db	4181171	CGTGGCGTGTTCGCGTTCGCGCTCATGTACACACCGACCGCGGTGTGACCCAGCTGTG	4181230
QY	422	ValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGluTyrIleAla	441
Db	4181231	GAAGCGCGCGCACCTGCACCTCGGCTTGGCACCGGGGAGTGTGTGGGAGATGCTCTCGCC	4181290
QY	442	ArgArgLeuArg	445
Db	4181291	TCAACATTGGCG	4181302

RESULT 4

US-09-103-840A-1
Sequence ID: Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 7,12e-51 Length: 4411529
Score: 591.00 Matches: 167
Percent Similarity: 50.86% Conservative: 69
Best Local Similarity: 35.99% Mismatches: 174
Query Match: 24.30% Indels: 54
DB: 3 Gaps: 12

US-09-963-521-2 (1-489) x US-09-103-840A-1 (1-4411529)

QY 7 LeunrGGLyATgLLeserThrVAlAspAlAlAlaAlaProProPseSerProLeu 26
Db 4187750 CTGGCGGGGCGC-----CGCATCCGCTGCCCGTG 4187779
QY 27 AlAProIleAspLeuThrAspHisSerGlnValAlaGly-----39
Db 4187780 GCG-----GGCGGGCGAGCGCCCTCGGAGATGATGACCTGCACACC 4187827
QY 40 -----ValMetAsnIleuAlAlAlaArgILeGlyAspILeuleuSerSerGlyThrSer 57
Db 4187828 CGGAAGGCTGTGACCTGCATCCATCCGGCTGCCAGAGATGATGTCTCGCTCGGC 4187887
QY 58 AsnSerAspThrIlyValGlnValArgAlaValThrSerAlaIlyGlyLeuYrTYrThr 77
Db 4187888 ACCGGGATGTGTGTGTGCACAGCCACGAGAGCTGTGCTCAGGCTCAGACTACCGATTGC 4187947
QY 78 HisValAspIleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgLys 97
Db 4187948 GTTTCGACATCACCCTTACCAACATC---ATCGTGTCCGCGTACGACACCAACACT 4188004
QY 98 MetProValAsnValPheHisValValGlyLysLeuAspThrAsnAspSerLysLeuSer 117
Db 4188005 CGCGCGGTACCATATATGCGGTGCTCGGACCGCGTCACTGACTACAGCGGCTGGCC 4188064
QY 118 GlnValAspArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGlnValAlaGln 137
Db 4188065 GAACTCGATCAGCTGTTCAAGGAGATACCTCCGGTGCCTGCGACGTGCACAGAGCTCAC 4188124
QY 138 LysIleLeuAspGlnLeuGlnIleAsnSerProAlaSerIlyGlyPheProValAlaLeu 157
Db 4188125 GAGGCTATGACGAGATTGACCGAAGCGCCACCCCTTACCGCGGTGCTGCGACCGCG 4188185
QY 158 GlyTPAlaMetMetGlyGlyAlaValAlaValLeuLeuGlyGlyIlyTPGlnValSer 177
Db 4188185 GGCGCGCGGCGCTTGCACCTCGCGCTCCCATGTGTCTCGCGGAGAACCTGCTGACTGC 4188244
QY 178 LeuIleAlaPheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysLys 197
Db 4188245 GTCTTGGCTGCGCTGACGCTGTGGCTGATCAGCCACACTGGCGGCTGCTGAACCGATTC 4188304
QY 198 GlyLeuProThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSer 217


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QY 182 ILeThrAlaPheThrIleIleAlaThrSerPheLeuGlyLysGlyLeuProThr 201
DB 8211 ATTGGCGGGAGATCCCATTTTAAACATTCAGCTTGTGCAAGCTATATACAAATTAA 8152
QY 202 PhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyrSer 221
DB 8151 TTTTCTCAGAG-----TTTGTGCA-----GCCGCTGTCGTCATATCC 8113
QY 222 LeuAlaLeuGlnPhe-----GlyLeuGlnIleLysProSerGlnIleIleAlaSer 238
DB 8112 ATTGCACCCCATTTACTTAATTAAGATGCAACCAATACAGATATCACTTACTATAGCC 8053
QY 239 GlyIleValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThr 258
DB 8052 AGTGCATATGCACCTGCTCCCTGATATTAATTAACCAATCCATTCAGAGTTATTAAGCG 7993
QY 259 GlyAlaProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIle 278
DB 7992 GGTGAATTAATCTTGAGGTATGCTCGCGGTGAGCTGCATTAACAGATTCGCATC 7933
QY 279 ValAlaGlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuHisValMetLeuProAla 298
DB 7932 GGTGCTGCTGTCGATC-----GTTTATTA----- 7906
QY 299 MetGlnSerAlaAlaAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyIle 318
DB 7905 -----ATCATTTAAGAGAG 7891
QY 319 ValThrAlaAlaAlaPheAlaVal-----GlyCysTyrAlaGluTyr 332
DB 7890 ACTGTTAAACGATGCTATTTTATTATTATTCATTACATCAGCTTATTAACAGATAC 7831
QY 333 SerSerValIleIleIle-----AlaGlyLeuThrAla 342
DB 7830 TTTTCTCT-ATCATTTCATATGCAACCAAGCCTTGAAGATGAGATTTGTGGGT 7772
QY 343 LeuMetGlySerAlaPheTyrTyrLeuPheVal---ValTyrLeuGlyProValSerAla 361
DB 7771 GCCATTGCATGAGCATTTTACCAATTAACGATTAATTAAGATTGGAAGATGGCGCT 7712
QY 362 AlaAlaIleAlaIleAlaThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgPheLeu 381
DB 7711 TCATTTTGGAGACTTAATTTAGGCTTAATGAGTCACTACTAGACGCGAGATATAA 7652
QY 382 IleProPheLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAlaIle 401
DB 7651 CGACCCGTAATTAATTAATGATAGTGCACGACATTAACATTAGTACCTGCTGTCAGCT 7592
QY 402 TyrArgGly---MetTyrAlaThrLeuAsnAspGlnThr 413
DB 7591 TATCAGCGACTGCTTTTATGATCAAAATGATATATA 7553

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RESULT 6
US-08-961-527-87/C
Sequence 87, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

```

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEO ID NO: 87
SEQUENCE CHARACTERISTICS:
LENGTH: 18436 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-87
Alignment Scores:
Pred. No.: 2.68e-07 Length: 18436
Score: 169.50 Matches: 106
Percent Similarity: 37.00% Conservative: 79
Best Local Similarity: 21.20% Mismatches: 195
Query Match: 6.97% Indels: 123
DB: Gaps: 16
US-09-963-521-2 (1-489) x US-08-961-527-87 (1-18436)
QY 31 LeuThrAspHisSerGlnValAlaGlyValMetAsnLeuAlaAlaArgIleGlyAspIle 50
DB 7209 ATGGAAGAAATCAAAAGATTAATTAATCCGCTCATGATGTGATTAATGACGGGAGCATTT 7150
QY 51 LeuLeuSerSerGlyThrSer-----AsnSerAspThrLysValGlnValArgAla 67
DB 7149 CTCCTTAAAGTGGCTCAGAAATCATCATCGTGTAGAAAGATCCAGATTCGATC----- 7096
QY 68 ValThrSerAlaTyrGlyLeuTyrTyrThrHisValAspIleThrLeuAsnThrIleThr 87
DB 7095 -----GCGCAATTCGACAGGGATTTGGATTCGATGCTGCTGCCATCCCTGCCCT 7045
QY 88 IlePhe-----ThrAsnIleGlyValGluArgLysMetProValAsnVal 102
DB 7044 ATCTTTTCTCTATGAAAAATACCAATATTGGCGCAG-AGCGCGTACCTCCTTCT 6986
QY 103 PheHisValValGlyLysLeuAspThrAsnPheSerLysLeuSerGluValAlaAspArgLeu 122
DB 6985 TAT-----AACATCGAAAAAGCTCGGATGTGAACCGATT 6950
QY 123 IleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGluLysIleLeuAspGlu 142
DB 6949 TCTGCTAGCTAGTTGGGGGGCAGATTGACTTAGAAACAGCTTTAAGCATTTGACGGCC 6890
QY 143 LeuGlnGlnSerProAlaSerTyrGly-----TyrAlaMetMetGlyGlyValAla 151
DB 6889 TTGCAGCGCAAAACCCCTTCCTATATCTAAGTTGACAGTAAATATCTACAGCAGCTGGGCGAGAGTG 6770
QY 152 -----PheProValAlaLeuLeuGly-----TyrAlaMetMetGlyGlyValAla 166
DB 6829 GCTCCTTCTTTTTCAGTATATGTTTAGCGGAATATCTACAGCAGCTTGGGCGAGAGTG 6770
QY 167 AlaValIleLeuLeuGlyGlyGlyThrGlnValSerLeu-----IleAlaPhe 181
DB 6769 GCGACCTTATTTGTTTGGCTTTTCCCTCATGTGGAATAATTTATCCGATTCCTTT 6710
QY 182 IleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysGlyLeuProThr 201
DB 6709 GTGACAGCTTT----- 6698
QY 202 PhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyrSer 221

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Db      6697  -----GCTGAGCCTTGTCTTTGGGATA-----ATTGCCCAAGTT 6662
QY      222  LeuAlaLeuGlnPheGlnLeuGlnLeuPheSerGlnLeuLeuAlaSerGlyLeuVal 241
        |||
Db      6661  TGGGCTCGCAACAGGTTTTCCTCAACGCGCAATTGATTATAGCTGGTGGCTATG 6602
QY      242  ValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyLeuThrGlyAlaPro 261
        |||
Db      6601  CCGTTGTACCAAGTATGCTTGAACCAACGCGTCCGATATTATGACCAACCAATA 6542
QY      262  ValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyLeuValAlaGly 281
        |||
Db      6541  AACCTGGATGAGTAAGATGTTGAATCCCTGCTCAATCCCTGCTTAAAGGGGACGA 6482
QY      282  ValGlyLeuGlyLeuGlnLeuSerGlnLeuHisValMetLeuProAlaMetGlnSer 301
        |||
Db      6481  ACTTCGTGCTGCTTGGT-ATTGATGAACATAATATG-ACACTAACACACTTTTATTACAA 6424
QY      302  AlaAlaAlaProAsnTySerSerThrPheAlaArgLeuLeuAlaGlyValThrAla 321
        |||
Db      6423  GCAGTAGCA-----AGTTTCTTGCCATTATC----- 6397
QY      322  AlaAlaPheAlaValGlyCysTyrrAlaGlnTrpSerSerValLeuLeuAlaGlyLeuThr 341
        |||
Db      6396  ---ACTTTTAAATTCGACTCAATGTCACACGCTTATGCTTACCTGAGGAGATTG 6340
QY      342  AlaLeuMetGlySerAlaPheTyrrTyrrLeuPheValValTyrrLeuGlyProValSerAla 361
        |||
Db      6339  GGCATACAGCTCGGCAATCTATCTCTCTGCTCAAGAACCGCAACATGCAATTGATGCT 6280
QY      362  AlaAlaIleAlaAlaThrAlaValAlaGlyPheThrGlyLeuLeuAlaArgArgPheLeu 381
        |||
Db      6279  ACCCTTATGACACCTTATGTTGCTGTGTCAGCAGATTTAATGATCTTTTAAAG 6220
QY      382  IleProLeuLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAlaIle 401
        |||
Db      6219  AACCTGCTGTGCTCTTATCTTGGCCATTGTCACCGCTGCTCAGGTTATCTCTCC 6160
QY      402  TyrArg-----GlyMetTyrrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsn 419
        |||
Db      6159  TACCGAACAACTGCTTTTGTGACA-----GGGACATAATAT 6121
QY      420  IleAlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGlnTr 439
        |||
Db      6120  AAAGCACTGCGAAGTCGACCTGTTGATGTTGCTTGGTATCTCTATTGGAATG 6061
QY      439  PheLeuAla-----ArgArg 443
        |||
Db      6060  GCTAGCGGACAGTATCTCAGACTCTATCATTTATATATAAAACACATGAGATGCTAG 6001
QY      443  GlnLeuArgArgProProArgPhe----- 450
        |||
Db      6000  ACTTTACAGAAATAAAGAAATTTTCGAAAAATGAGATAAATTAATGATAACGCTTCT 5941
QY      451  -----AsnProTyrrArgAlaPheThrLys--AlaAsnGlnPheSerPheGlnGlu 466
        |||
Db      5940  ATATGTGCGAAGATACCGCACTTATGAGAAATGCGGCTGATTTGGTATCCAGCAA 5883

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; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 23210
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 28
; OTHER INFORMATION: a or g or c or t, unknown, or other
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte template ID No. 6632636 17
; PUBLICATION INFORMATION:
US-09-596-002-17

Alignment Scores:
Pred. No.: 1.26e-06 Length: 23210
Score: 165.00 Matches: 95
Percent Similarity: 37.84% Conservative: 84
Best Local Similarity: 20.08% Mismatches: 207
Query Match: 6.78% Indels: 88
DB: 4 Gaps: 14

US-09-963-521-2 (1-489) x US-09-596-002-17 (1-23210)

QY      13  ThrValAspAlaIleAlaValAlaProProSerProLeuAlaProIleAspLeuThr 32
        |||
Db      22074  ACCATTCAAGCCACCAAAAGTCACCA-----ATGACTAATTTGACC 22033
QY      33  Asp-----HisSerGlnVal 37
        |||
Db      22032  GACGAGATGCCACGATTTTATTGATACGCATACACGCCGCTTAACATATGCTACGCA 21973
QY      38  AlaGlyValMetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerGlyThrSer 57
        |||
Db      21972  CAAAGATACCTGCTTATGATATCCGCTGCTTACTACTCATCAATGATAGTGACAG 21913
QY      58  AsnSerAspThrLysValGlnValAlaValAlaThrSerAlaTyrrGlyLeuTyrrThr 77
        |||
Db      21912  TCTGTCGTGCTGCTTATTAACAAAGCGGCTTGGGCGGCACTTGAGATGATGCTGT 21853
QY      78  HisValAspIleThrLeuAsnThrIleThrIlePheThr----- 90
        |||
Db      21852  GAGTCGGTTCGATTTAATGCGGTACCTTAACCACTTATATACAGTCGCTGATAC 21793
QY      91  -----AsnIleGlyValGluArgLysMetProValAsnValPhe 103
        |||
Db      21792  ACAACGTCGAGAAATACCGTTCATCAAGCAATTAATGTCAGATCTTAGTACAAATTTCA 21733
QY      104  HisValValGlyLysLeuAspThrAsnPheSerLysLeuSerGlnVal----- 119
        |||
Db      21732  CAAATTTATCTTAAGCGCGCAAAATCATCAAGCAATCAATCTGATTTGTTAAACCCCA 21673
QY      120  -----AspArgLeuIleArgSerIleGlnAlaGlyAlaThrProGlnValAlaGlu 137
        |||
Db      21672  AGCCATGACGCAATGATATAGTACGATGCAAGG----- 21637
QY      138  LysIleLeuAspGlnLeuGlnLeuSerPro-----AlaSerTyrrGlyPhe 152
        |||
Db      21636  -----TTTGATGCCATCTACCAAACTGCTATCTAATCATTTGGTATGTTTGTG 21583
QY      153  ProValAlaLeuLeuGlyTyrrAlaMetMetGlyGlyAlaValAlaValLeuLeuGlyGly 172
        |||
Db      21582  GCGCATATCATGCGCAGTTTCCATTATTAACGTCACACTTGGTG----- 21535
QY      173  GlyTyrrGlnValSerLeuIleAlaPheIleThrAlaPheThrIleIleAlaThrThrSer 192
        |||
Db      21534  -----ATTGCTCTGATTACTTTATTTGGCAGATTTTGTTCGATGAGATGGGTG 21484
QY      193  PheLeuGlyLysLysGlyLeuProThrPhePheGlnAsnValValGlyGlyPheIleAla 212
        |||
Db      21483  TATCTTTAAAGCAACATTTTAATCTTTTGTGCTGCTATGATGACGCAATTTACCGCA 21424

```

```

RESULT 7
US-09-596-002-17/c
; Sequence 17, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18

```



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QY      213 ThrLeuProAlaSerIleAlaTyrSerLeuAlaLeuGlnPheGlyLeuGlnIleLysPro 232
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      21423 ACTTATTTGGCAGCTTTGGCATTTTATTAAATTAGTAACTAATGCTGACATTT----- 21370
QY      233 SerGlnIleAlaSerGlyIleValIleLeuAlaGlyLeuThrLeuValGlnSer 252
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      21369 -----GCTGTCCCTCCAGCTGCTGCTATTACTTGTACCAAGCTTCCCTATTATATGCG 21316
QY      253 LeuGlnAspGlyIleThrGlyAlaProValThrAlaSerAlaArgPheGluThrLeu 272
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      21315 TTATCGGATATCTTAAAGGCTATGATGATGAGGCGTAGTGCATGATGATTTGCAACC 21256
QY      273 LeuPheThrGlyIleValAlaGlyValGlyLeuGlyIleGlnLeuSerGluIleLeu 292
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      21255 ATGCTAACCTTATCAGCTGCTGTTGGATTTGATGACCTTGATTTTCTTAAGATTTCA 21196
QY      293 HisValMetLeu---ProAlaMetGlnSerAlaAlaAlaProAsnTyrSerSerThrPhe 311
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      21195 CATTGGGAGCTATGATGAGGCTATATCGAGTTATCCAAACATTTGAT-----TGTGAT 21142
QY      312 AlaArgIleIleAlaGlyIleVal-----ThrAlaAlaAlaPheAlaValGlyCysTyr 329
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      21141 GTATCATTTACTGTGGCTGGTGTATGTTTACATTCAGCCAAAGCATATCATGATGATT 21082
QY      330 AlaGluTyrSerSerValIleIleAlaGlyLeuThrAlaLeuMetGlySerAlaPheTyr 349
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      21081 GCATGATGCTAACGACGACTTGCTTTT-GGTTTAAACACAGTGAG----- 21038
QY      350 TyrLeuPheValValTyrLeuGlyProValSerAlaAlaAlaIleAlaAlaThrAlaVal 369
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      21037 GTACCTTTGGTGTGCTGCTG-----GTTGTGCAACATTTCTTTGGGGGATGCGGGGT 20984
QY      370 GlyPheThrGlyGlyLeuLeuAlaArgArgPheLeuIleProPheLeuIleValAlaIle 389
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      20983 AGCTTTTGGGTGACATTTTGTCTCAGGTCATGCGCTGCTTAAAGCTTATTTGTA 20924
QY      390 AlaGlyIleThrProMetLeuProGlyLeuAlaIleTyrArgGlyMetTyrAlaThrLeu 409
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      20923 CCTAGCTGATTGTGATGATGCTCGGGAATCGCTCCTATTAAGCATGATGATGTA 20864
QY      410 Asn-----AspGlnThrLeuMetGlyPheThrAsnIleAla 421
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      20863 CAATTTGGCTATTTGGATTTGATATGATGATTTATTTATCGTTATGANGCGCATTTT 20804
QY      422 ValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyVal 434
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      20803 GAGCGCATTTTATCATCTCAGCATTTGGTTTGGGGCTG 20765

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```

RESULT 8
US-09-252-991A-6186
; Sequence 6186, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OR INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6186
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6186

```

Alignment Scores: 7,58e-07 Length: 912
Pred. No.: 146.50 Matches: 76

Percent Similarity: 32.69%
Best Local Similarity: 24.60%
Query Match: 6.02%
DB: 4
Gaps: 8

US-09-963-521-2 (1-489) x US-09-252-991A-6186 (1-912)

```

QY      151 GlyPheProValAlaLeuLeuGlyTyrAlaMetMetGlyIleValAlaValIleLeu 170
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      173 GGGTTTGCAGACAGCCCTTTAGAGGCGCTGTCGGGGGGGGCGCTTGGTCC-----CGC 229
QY      171 Gly-GlyGlyTyrGlnValSerLeuIleAlaPheIleThrAlaPheThrIleIleAla 190
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      230 GCGAGCGCTTGCAGACAGCGCTGAGCGCGCTGCCGGGGCGCTGCGAGTCCGCCAGG 289
QY      190 ThrSerPheLeuGlyIleValGlyLeuProThrPhePheGlnAsnValAlaGlyIlePh 210
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      290 CTTCGAGCAGGAGCGGCTGGCGGCTTG-----GTTCCGCAAGCTTT 331
QY      210 eIleAlaThr---LeuProAlaSerIleAlaTyrSerLeuAlaLeuGlnPheGlyLeu 229
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      332 CGCGGCTACGGGTTTCCCGCAGGCTTGGCGCGGTTTCCCGCAGGCTTC----- 383
QY      229 uIleLysProSerGlnIleIleAlaSerGlyIleValIleLeuAlaGlyLeuThrLe 249
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      384 -----GCAGCGGCTTGGCTGACGCTTCCGCGCGGCGGATTT 421
QY      249 uValGlnSerLeuAlaAspGlyIleThrGlyAlaProValThrAlaSerAlaArgPhePh 269
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      422 CGCCACAGGCTTGGCGCGGCTTTCGCCGAGCTTCCAGCTTGGCTGGCGGCTT 481
QY      269 eGluThrLeuPheThrGlyIleValAlaGlyValGlyLeuGlyIleGlnLeu 289
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      482 CGCGGCTGCGGTTTTCGCCGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGG 541
QY      289 rGluIleLeuHisValMetLeuProAlaMetGlnSerAlaAlaAlaProAsnTyrSer 309
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      542 CTTCGCGCGGCTTCCGCGCTGCGGCTTTCGCCGAGCTTGGCGCGGCTTTCGCCAC 601
QY      309 rThrPheAlaArgIleIleAlaGlyIleValThrAlaAlaPheAlaValGlyCysTyr 329
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      602 AGCTTTCGCGCGGCTTGGCTTGGCGGCTTTCGCCGCTTTCGCCGCGGCTTTCGCC 661
QY      329 rAlaGluTyrSerSerValIleIleAlaGlyLeuThrAlaLeuMetGlySerAlaPheTyr 349
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      662 CGCGGCTTTCGACAGGCTTCCGCGCTTGGCTTGGCGGCTTTCGCCGCGGCTTTC 721
QY      349 rTyrLeuPheValValTyrLeuGlyProValSerAlaAlaAlaIleAlaThrAlaVal 369
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      722 C-----GCCGACAGCTTGGCGCGGCTTTCGCCAGC 751
QY      369 lGlyPheThrGlyLeuLeuAlaArgArgPheLeuIleProPheLeuIleValAlaIle 389
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      752 AGGCTTGCAGCGCGGCTTGGCGGCA----- 776
QY      389 eAlaGlyIleThrProMetLeuProGlyLeuAlaIleTyrArgGlyMetTyrAlaThrLe 409
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      776 ----- 776
QY      409 uAsnAspGlnThrLeuMetGlyPheThrAsnIleAlaValAlaLeuAlaThrAlaSerSe 429
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      777 -----GGCTTGCCTACAGCTTTCACCGAGGCTTGGCTGCGCCG 817
QY      429 rLeuAlaAlaGlyValAlaLeuGlyGluTyrIleAlaArgArgLeuArgProProAla 449
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      818 CTTCGACAGGCTTGGCTGCGGCTT-----TTGCGCTTGGCGGCTTCCAGAGCC----- 866
QY      449 gPheAsnProTyrArgAlaPheThr 457
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      867 -----TTGCCAGAGCTTCTTCAC 887

```

RESULT 9
US-09-252-991A-6445/c

```
; Sequence 6445, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6445
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-6445
```

```
Alignment Scores:
Pred. No.: 7,62e-07 Length: 915
Score: 146.50 Matches: 76
Percent Similarity: 32.69% Conservative: 25
Best Local Similarity: 24.60% Mismatches: 136
Query Match: 6.02% Indels: 72
DB: 4 Gaps: 8
```

US-09-963-521-2 (1-489) x US-09-252-991A-6445 (1-915)

```
QY 151 G1YPheProValAlaLeuLeuGlyTTPAlaMetMetGlyGlyAlaValAlaValLeuLeu 170
Db 754 GGCTTTCAGACAGCGCTTAGAGGCGCTGTCGGGCGCGCGCTTGTCTGCC---CGC 698
QY 171 G1Y-G1Yg1YTrpGlnValSerLeuIleAlaPheIleThrAlaPheThrIleIleAla 190
Db 697 GGCAGCGCTTGCAGAGCGCGCTGAGGCGCTGCCCGCGCGCTGGAGTTCGCCGAGG 638
QY 190 rThrSerPheLeuGlyLysLysGlyLeuProThrPhePheGlnAsnValAlaGlyLys 210
Db 637 CTTCGACAGCAGCAGCGTGGCGGCTTGTG-----GTTGCGGACAGGTTT 596
QY 210 e1leAlaThr---LeuProAlaSerIleAlaTyrrSerLeuAlaLeuGlnPheGlyLeuG1 229
Db 595 CGCGGCTTACGGGCTTTCGCCGAGCTTGGCGCGCTTTCGCCGAGGCTTC----- 544
QY 229 u1leLysProSerGlnIleIleAlaSerGlyIleValAlaValLeuLeuAlaGlyLeuThr 249
Db 543 -----GCAAGCGCTTGGCTGCGAGGCTTGGCGCGCGCGGCGGATTT 506
QY 249 uValGlnSerLeuGlnAspGlyIleThrGlyAlaProValThrAlaSerAlaArgPhe 269
Db 505 CGCGCAGAGGCTTGGCGCGGCTTTCGCCGAGGCTTTCGAGCTTGGCTTGGCGGCTT 446
QY 269 eGlnThrLeuLeuPheThrGlyGlyIleValAlaGlyValAlaGlyLeuGlyIleGlnLeu 289
Db 445 CGCGGCTTGGCTTTCGCCGCGGCTTGGCGCGCTTTCGCCGAGGCTTTCGCCCGG 386
QY 289 rGlnIleLeuHisValMetLeuProAlaMetGlnSerAlaAlaAlaProAsnTyrSer 309
Db 385 CTTCGCGGCGGCTTTCGCCGCTTTCGCCGAGGCTTTCGCCGCGGCTTTCGCCCG 326
QY 309 rThrPheAlaArgIleIleAlaGlyGlyValThrAlaAlaAlaPheAlaValAlaGly 329
Db 329 rAlaGlnTrpSerSerValIleIleAlaGlyLeuThrAlaLeuMetGlySerAlaPhe 349
QY 349 rTyrLeuPheValValTyrLeuGlyProValSerAlaAlaAlaAlaAlaThrAlaVal 369
Db 205 C-----GCCGAGGCTTGGCTGCGAGGCTTTCGCCGAGGCTTTCGCCGAGC 176
```

```
QY 369 1G1YPheThrGlyLysLeuLeuAlaArgPheLeuIleProProLeuIleValAlaI 389
Db 175 AGGCTTTCAGACCGCGCTTGGCGCGA----- 151
QY 389 eAlaGlyIleThrProMetLeuProGlyLeuAlaIleTyrrArgGlyMetTyrrAlaThr 409
Db 151 ----- 151
QY 409 uAsnAspGlnThrLeuMetGlyPheThrAsnIleAlaValAlaLeuAlaThrAlaSer 429
Db 150 -----GCTTCGCCGCTTACCGGCTTTCACCGCAGGCTTGGCTTGGCGCGC 110
QY 429 rLeuAlaAlaGlyValValLeuGlyLysIleAlaArgPheLeuArgPheProPhe 449
Db 109 CTTCGACAGCAGGCTTTCGCCGCTTTCGCCGCTTTCGCCGCTTTCGCCGCTTTCGCC 61
QY 449 gPheAsnProTyrArgAlaPheThr 457
Db 60 ----TTGCCAGCAGGCTTCTTCAAC 40
```

RESULT 10

US-09-252-991A-6023
Sequence 6023, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 6023

LENGTH: 1806

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-6023

Alignment Scores:
Pred. No.: 2,32e-06 Length: 1806
Score: 146.50 Matches: 76
Percent Similarity: 32.69% Conservative: 25
Best Local Similarity: 24.60% Mismatches: 136
Query Match: 6.02% Indels: 72
DB: 4 Gaps: 8

US-09-963-521-2 (1-489) x US-09-252-991A-6023 (1-1806)

```
QY 151 G1YPheProValAlaLeuLeuGlyTTPAlaMetMetGlyGlyAlaValAlaValLeuLeu 170
Db 517 GGCTTTCAGACAGCGCTTTCAGAGGCGCTTGGCGCGGCTTTCGCCGCTTTCGCC 573
QY 171 G1Y-G1Yg1YTrpGlnValSerLeuIleAlaPheIleThrAlaPheThrIleIleAla 190
Db 574 GGCAGGCGTTCGCGAGGCGCTGAGGCGGCTGCGGCGGCTGCGGAGTTCGCCGAG 633
QY 190 rThrSerPheLeuGlyLysLysGlyLeuProThrPhePheGlnAsnValAlaGlyLys 210
Db 634 CTTCGACAGCAGCAGCGTGGCGGCTTGTG-----GTTGCGGACAGGTTT 675
QY 210 e1leAlaThr---LeuProAlaSerIleAlaTyrrSerLeuAlaLeuGlnPheGlyLeuG1 229
Db 676 CGCGGCTTACGGGCTTTCGCCGAGGCTTTCGCCGAGGCTTTCGCCGAGGCTTC----- 727
QY 229 u1leLysProSerGlnIleIleAlaSerGlyIleValAlaValLeuLeuAlaGlyLeuThr 249
Db 728 -----GCAAGCGCTTGGCTGCGAGGCTTTCGCCGAGGCTTTCGCCGAGC 176
```

QY 249 uValGlnSerLeuGlnAspGlyLeThrGlyAlaProValThrAlaSerAlaArgPhe 269
Db 766 CGCCACAGAGCTTGGCCGCGCTTCCGCCGACAGCTTCGACAGCTGAGCTTGGCTTCGCGCTT 825
QY 269 eGlnThrLeuLeuPheThrGlyGlyLeValAlaGlyValGlyLeuGlyLeuGln 289
Db 826 CGCGGCTGCGGTTTGGCCGCGGAGCTTGGCTTGGCCGACAGCTTGGCTTCGCGCTT 885
QY 289 rGluLeuLeuValMetLeuProAlaMetGlnSerAlaAlaProAlaSerLeu 309
Db 886 CTGGGCGCGGCTTGGCCGCTTGGCTTGGCCGACAGCTTGGCTTGGCTTGGCTTGGCC 945
QY 309 rThrPheAlaArgIleLeuAlaGlyValThrAlaAlaPheAlaValGlyCys 329
Db 946 AGGCTTCGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGC 1005
QY 329 rAlaGlnTrpSerSerValIleIleAlaGlyLeuThrAlaLeuMetGlySerAlaPhe 349
Db 1006 CGCGGCTTGGCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 1065
QY 349 rTyrLeuPheValValTyrLeuGlyProValSerAlaAlaIleAlaAlaThrAla 369
Db 1066 C-----GCCGACAGCTTGGCGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGAGC 1095
QY 369 lGlyPheThrGlyGlyLeuLeuAlaArgArgPheLeuLeuProProLeuLeuAlaAla 389
Db 1096 AGGCTTCGCGAGCTTGGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGC 1120
QY 389 eAlaGlyIleThrProMetLeuProGlyLeuAlaIleTyrArgGlyMetTyrAlaThr 409
Db 1120 ----- 1120
QY 409 uAsnAspGlnThrLeuMetGlyPheThrAsnIleAlaValAlaLeuAlaThrAlaSer 429
Db 1121 -----GGCTTCGCGCGCTTGGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGC 1161
QY 429 rLeuAlaAlaGlyValValLeuGlyGlyIleThrAlaAlaArgArgLeuArgArgPro 449
Db 1162 CTTCGCGAGAGCTTGGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCG 1210
QY 449 gPheAsnProTyrArgAlaPheThr 457
Db 1211 -----TTGCCACAGCTTCTTCACCT 1231

RESULT 11
US-09-107-532A-248
Sequence 248, Application US/09107532A
Patent No. 6583375
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Atinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 248:
SEQUENCE CHARACTERISTICS:
LENGTH: 1896 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (b) LOCATION 1...1896
SEQUENCE DESCRIPTION: SEQ ID NO: 248:
US-09-107-532A-248

Alignment Scores:
Pred. No.: 5,47e-06 Length: 1896
Score: 143.50 Matches: 98
Percent Similarity: 37.73% Conservative: 68
Best Local Similarity: 22.27% Mismatches: 162
Query Match: 5.90% Indels: 113
Gaps: 21

US-09-963-521-2 (1-489) x US-09-107-532A-248 (1-1896)

QY 88 lPheThrAsnIleGlyValGluArgLysMetProValAsnValPheHisValValGly 107
Db 107 ATATTGTCGATTTGTGCGAGCGAGAAATGTCACG-AAATGTTTACCATTTGCGACA 165
QY 108 LysLeu-----AspThrAsnPheSerLysLeuSerGluVal 119
Db 166 AGGTTAGCGCTTACCTTAAGAAATATAGAAAGCAGATATAGAGAAAGCTAGACCACTA 225
QY 120 AspArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGluLysIle 139
Db 226 GAAGTGTGATCATGTAGTCGAAGCTGAGAAATGTTCAAGTCGTAAGTATGAGAAATGCA 285
QY 140 LeuAspGlu-----LeuGlnGlnSerProAlaSer 149
Db 286 GTAATGAAAGTATGACGATATATCCAAACAAATGAAACTAGAAAGATGATGATGATGAT 345
QY 150 -----TyrGlyPheProValAlaLeuLeuGlyTyr-----Ala 160
Db 346 GGAAGAGAGCACTGAGAAAGCACTTTTAACTCTTTTATATGACATGATGCGCGCT 405
QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyTyrGlnValSerLeuIleAla 180
Db 406 GTTTTGGCCCGACCTTAGCGGCTTGGCAGAAAGTGTGATCAAGAGATCTGCGC 465
QY 181 PheIleThrAlaPheThrIleIleAlaThrPheSerPheLeuGlyLysGlyLeuPro 200
Db 466 TTATGTACAGAGTTGAAATTTATTACTGCTGAAATCA-----GGAACCTAT 510
QY 201 ThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr 220
Db 511 ATCATTTTGATGCGAGCGATGATGATGATTTTCTATTTCTGCTATATTTTGGCAAT 570
QY 221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLysProSerGlnIleIleAlaSerGlyIle 240
Db 571 ACTGCTGCAAAAAGTTCATACAGAT-----CGTTTCATGCTATGTTAT 618
QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThr----- 258
Db 619 GCAGAGCTTCTGTTATCTTACGATGTCAGTATGATGATGATGATGATGATGATGATGATGAT 678

PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 7755
 LENGTH: 1581
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-7755

Alignment Scores:
 Pred. No.: 5,276-06 Length: 1581
 Score: 142.50 Matches: 127
 Percent Similarity: 35.00% Conservative: 69
 Best Local Similarity: 22.68% Mismatches: 175
 Query Match: 5.86% Indels: 190
 DB: 4 Gaps: 26

US-09-963-521-2 (1-489) x US-09-252-991A-7755 (1-1581)

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 32 rAspHisSerGlnValAlaGlyValMetAsnLeuAlaArgIleGlyAspIleLeu 52
 93 GCGACATGCTGCG-----CTGGCTGAAGGAACCGGAGAGACTTCG 134
 52 userSerGlyThrSerAsnSerAspThrIlySvalGlnValArgAlaValThrSerAlaIy 72
 135 TCAGAGCAGACCAACCGCTTGAGATCGCGCTGCGC---CGGCAAGTTCCAGCAGCGTA 191
 72 r-GlyLeuIyrrYrThrHisValAspIleThrLeuAsnThrIleThrIlePheThrAsnI 92
 192 CCGGTCTCTCCAGCTCCACCGTATCGGTACACCTCGCACCTG----- 235
 92 IeGlyValGlnArgIlyMetProValAsnValPheHisValIleGlyIlySerLeuAspThra 112
 236 -----CAACGGCCGGCTGTGGTACACCGCCGGGTGGCCAG-----TGA 278
 112 snpSerIyIyLeuSerGlnValAspArgLeuIleArgSerIleGlnAla----- 128
 279 ACTTCTTCAAGCGCAACGAG-----GAGACCATCCAGGCTTCTCTCGAC 323
 129 -----GlyAlaThrProProGlnValAlaGlnIlysi 139
 324 AACTCGCGACGAGCTGTAGCAGCAGCTGCTTCCACCCACCA----- 367
 139 IeLeuAspGlnLeuGlnGlnSerProAlaSerIyGlyIyPheProValAlaLeuLeuGlyI 159
 368 -----CTTCGAGTCCAGAGAGCTCGACGAGATGCGCGCTCTCTTCGTC 413
 159 rPalameMetGlyIyAlaValAla-----ValLeuLeuGly----- 171
 414 TCGCTTATCGCGCTTTCGATCGGTACACCGAATTCGATCATGGGCGCTGCGCCG 473
 172 -----GlyGlyThrGlnValSerLeuIleA 180
 474 AGGTCCGCGGACCTGCGGTATCCATCCAGCGCGGCTGCTGTATCAGCGGCTAG 533
 180 IapheIleThrAlaPhe-----ThrIleIleAlaThrThrSerPheLeuGlyI 196
 534 CCTTCGCGGTGGCTTCGCGCGCCCGCGATGGCGACGCGCCGCGTGGAGCGCA 593
 196 yslYsglyLeuProThrPhePheGlnAsnValAlaGlyIyPheIleAlaThrLeuProA 216
 594 AGAAGACCTGCTCGCG-----CTGATGGGATCTTCTATCTCTC-----G 632
 216 IasertIleAlaIySerIleuAlaLeuGlnpGlyLeuGlnIleIySerProSerGlnIleI 236
 633 GCAACTCTCTCGCGCGGTGGCGCAACTACGAGCTG----- 670
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 708 GC-----GCCCTTCTCGC-----ATCG 725
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 726 GCTCGGTGGTGGCGCGC----- 742
 296 euProAlaMetGlnSerAlaAlaAlaProAsnIySerSerThrPheAlaArgIleIleA 316
 743 -----AGCTGGTGGCGCGCAACCGCAGCGCTTCCGCGTGGCCCTGATGT 788
 316 IeGlyIyValThrAlaAla-----AlaPheAlaValAlaGlyCysr 329
 789 TCACCGGCTGACCGCTGGCCCAACGCTGCTGGCGCTGCCGCTGATCCGCGCTGGCCAG 848
 329 yzAlaGlnIyPseSer-----ValIleIleAlaGlyLeuThrAlaLeuMetG 345
 849 AAGCCGGCTGGCGCGACCTTCTGGGTGTGACCTGATCGCGCTGGCTGCTGCTG 908
 345 IySerAla-----PheIyThrLeuP 352
 909 GCTTGGCCAGGCTGCTGCCAAGCAGCAGCGAGAGAAAGTGCAGCTCGCCCGCAGAA 968
 352 heValValIyLeuGlyProValSerAlaAlaAlaIleAlaIleAlaValAlaGlyPheT 372
 969 TGTCCGCGCTGAAGAACCGCTGCTGTGGTGGCTGCGGCGACACCGCTGCTG---TTGG 1025
 372 hrGlyIyLeuLeuAlaArgArgPheLeuIleProProLeuIleValAlaIleAlaGlyI 392
 1026 CCGCTCGATGTGCGCTGCTGTACTACCTGCGCGCGCTGCGGAGATCACCGGG 1085
 392 IeThrPro-----MetLeuProGlyLeuAla----- 400
 1086 TCAGCCCGCGCGCGGTGACCTGCAGCTGCTGATCGGTGGTGGCTGACCTGCGCA 1145
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 1146 AGCTGATCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1205
 420 IeAlaValAlaLeuAlaThrAla-----SerSerLeuAlaAlaG 433
 1206 CCGCATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1265
 433 IyValIleValLeuGlyIyIleThrIleAlaArgArgLeuArgArgProProArgPheAsnProT 453
 1266 AATACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324
 453 yzArgAlaPheThrIyAla-----AsnGlnP 462
 1325 AAGCTGTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1384
 462 heSerPheGlnGlnAlaIleGlnIleAsnGlnArgArgGlnArgIyArgProIyS 480
 1385 TTCAACGTGGCAACGCGCTGCGCGCTGCGGTGGCGGCGACGTCATGACCAACG 1440

RESULT 14
 US-09-252-991A-6891
 Sequence 6891, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27


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; LENGTH: 1941
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-963-521-2 (1-489) x US-09-252-991A-6728 (1-1941)

Alignment Scores:
Pred. No.: 1,246-05 Length: 1941
Score: 140.50 Matches: 107
Percent Similarity: 34.87% Conservative: 82
Best Local Similarity: 19.74% Mismatches: 189
Query Match: 5.78% Indels: 165
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QY 22 -----ProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGly 39
DB 1791 ATGACCGCGGCTTCG-----ACTACCATTCGCGCGCGCGCGCGCGGAC 1750
QY 40 ValMetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSer 59
DB 1749 GCTCCCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1690
QY 60 AspThrIleValGlnValAlaArgAlaValThrSerAlaTyrglyLeuTygThrHisVal 79
DB 1689 CAGCAACCGGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 1630
QY 80 AspIleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGluArgGlyMetPro 99
DB 1629 GGGCTGACCTTCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1594
QY 100 ValAsnValPheHisValValGlyLeuAspThrAsnPheSerIleLeuSerGluVal 119
DB 1593 -----GSCACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1570
QY 120 AspArgLeuIleArgSerIleGlnAlaGlyAlaThrProGluValAlaGluValIle 139
DB 1570 ----- 1570
QY 140 LeuAspGluLeuGlnGlnSerProAlaSerTyrglyPheProValAlaLeuLeuGlyTyr 159
DB 1569 TACGACGACCTTC-----TTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1534
QY 160 AlaMetMetGlyValAlaValAlaValLeuLeuGlyGlyTyrPdpGlnValSerIle 179
DB 1533 CTGATGCTCGGCTGACACGCGCATCTCGGCTTCATCGCGCGCGCGCGCGCGCGCTTCC 1474
QY 180 AlaPheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyValGlyLeu 199
DB 1473 ACCGACCTGCGGCGCATTTACTCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 1414
QY 200 ProThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIle--- 218
DB 1413 GCT-----CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1363
QY 219 ---AlaTySerLeuAlaLeuGlnPheGlyLeuGlnIleLeuProSerGlnIleIleAla 237
DB 1362 CCCAAATACCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCC 1303
QY 238 SerGlyIleValValLeu-----LeuAlaGlyLeuThrLeuValGlnSer 252
DB 1302 GGAAGGCTGATGACCTTCACGCGTGTCTTCGCGCATCGCGCGCGCGCGCGCGCGCGCG 1243
QY 253 LeuGlnAspGlyIleThrGlyAlaProValThrAlaSerAlaArgPhePheGluThrLeu 272
DB 1242 ATC-----GGGCTCCCGCGCGCATCTCGTCTCGGCGCGCGCGCGCGCGCGCGCTG 1189
QY 273 LeuPheThrGlyGlyIleValAlaGlyValGlyLeuGlyIleGlnLeuSerGluLeu 292

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QY 293 HisValMetLeuProAlaMetGluSerAlaAlaAlaProAsnTygSerThrPheAla 312
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QY 313 ArgIleIleAlaGlyGlyValThrAlaAlaAlaPheAlaValGlyCysTygAlaGluTyr 332
DB 1116 GCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1057
QY 333 -----SerSerValIleIleAlaGlyLeuThrAlaLeuMetGlySerAla 347
DB 1056 GCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 997
QY 348 PheTygThrLeuPheValValTygLeuGlyProValSerAlaAlaIleAlaAlaThr 367
DB 996 CTGATGTATCATCTTC-----GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 949
QY 368 AlaValGlyPheThrIleGlyLeuLeuAlaArgArgPheLeuIleProProLeuIleVal 387
DB 948 GACATC-----TCCGACGTGATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 895
QY 388 AlaIleAlaGlyIleThrProMetLeuProGlyLeuAlaIleTygArgGlyMetTygAla 407
DB 894 CTC-----GGCGTGAACATCTCG----- 877
QY 408 ThrLeuAsnAspGlnThrLeu-----MetGlyPheThrAsnIleAla----- 421
DB 876 ACCACCAACGACAAAGCGGTGTATGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 817
QY 422 -----ValAlaLeuAlaThrAlaSerSerLeu----- 430
DB 816 TCCAGCGCGTTCCTGGCGATGTCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 757
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QY 434 ValValLeuGlyGluTyrPheAlaAlaArgArgLeuArgArgProProArgPheAsnProTyr 453
DB 696 GTGATCATCGCGCATCTGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 644
QY 454 ArgAlaPheThrIleValAlaAsnGluPheSerPheGlnGluAlaGluGlnAsnGlnArg 473
DB 643 CGGCGACATCCA-----GGCGATCACTGGCGCGCGCGCGCGCGCGCGCGCGCG 599
QY 474 ---ArgGlnArgGlyAsnPro-----LysThrAsnGlnArgPheGlyValAsn 487
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QY 488 LysArg 489
DB 538 CGCGCG 533

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Search completed: July 31, 2004, 11:47:18
 Job time : 4823 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 31, 2004, 10:08:48 ; Search time 585 Seconds

(Without alignments)
4098.522 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
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Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	2432	100.0	1590	13	US-10-450-055-41	Sequence 41, Ap
4	2432	100.0	1909	9	US-09-951-536-3	Sequence 3, Appl
5	2432	100.0	1909	9	US-09-963-521-3	Sequence 3, Appl
6	2432	100.0	1909	9	US-09-934-721-3	Sequence 3, Appl
7	2432	100.0	1909	9	US-09-783-388-3	Sequence 3, Appl
8	2432	100.0	1909	10	US-09-951-535-3	Sequence 3, Appl
9	2432	100.0	1909	17	US-10-924-574-11	Sequence 11, Appl
10	2432	100.0	2817	9	US-09-951-536-1	Sequence 1, Appl
11	2432	100.0	2817	9	US-09-963-521-1	Sequence 1, Appl
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15	2432	100.0	2817	17	US-10-924-574-9	Sequence 9, Appl
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17	770	31.7	3010	14	US-10-058-945-1	Sequence 1, Appl
18	408	16.8	1659	15	US-10-156-761-4644	Sequence 4644, Ap
19	408	16.8	9025608	15	US-10-156-761-1	Sequence 1, Appl
20	230.5	9.5	9172	9	US-09-070-927A-65	Sequence 65, Appl
21	196.5	8.1	3632	16	US-10-398-221-3672	Sequence 3672, Ap
22	190	7.8	9834	8	US-08-781-986A-37	Sequence 37, Appl
23	188.5	7.8	9834	13	US-10-329-624-37	Sequence 37, Appl
24	188.5	7.8	1163020	16	US-10-398-221-10	Sequence 10, Appl
25	188.5	7.8	3011208	16	US-10-398-221-3058	Sequence 2058, Ap
26	178.5	7.3	2594	9	US-09-070-927A-187	Sequence 187, Ap
27	175.5	7.2	2731748	17	US-10-297-465A-1	Sequence 1, Appl
28	169.5	7.0	18436	13	US-10-158-844-87	Sequence 87, Appl
29	165	6.8	23210	13	US-10-672-787-17	Sequence 17, Appl
30	147.5	6.1	1266	13	US-10-282-122A-14916	Sequence 14916, A
31	147.5	6.1	12278	16	US-10-398-221-3886	Sequence 3886, Ap
32	147	6.0	9219	13	US-10-282-122A-12963	Sequence 12963, A
33	144.5	5.9	3309400	9	US-09-738-626-1	Sequence 1, Appl
34	143.5	5.9	63158	15	US-10-292-188-1	Sequence 1, Appl
35	143	5.9	1230	13	US-10-156-761-1	Sequence 1, Appl
36	141	5.8	9025608	15	US-10-156-761-1	Sequence 1, Appl
37	138.5	5.7	1059	13	US-10-282-122A-10631	Sequence 10631, A
38	138.5	5.7	135638	15	US-10-314-657-1	Sequence 1, Appl
39	137.5	5.7	1854	16	US-10-398-221-1040	Sequence 1040, Ap
40	137.5	5.7	1854	16	US-10-398-221-2857	Sequence 2857, Ap
41	136	5.6	1863	13	US-10-282-122A-38255	Sequence 38255, A
42	134.5	5.5	1647	15	US-10-156-761-6431	Sequence 6431, Ap
43	134.5	5.5	2112	15	US-10-156-761-3675	Sequence 3675, Ap
44	134.5	5.5	2731748	17	US-10-297-465A-1	Sequence 1, Appl
45	134	5.5	1128	9	US-09-738-626-2689	Sequence 2689, Ap

ALIGNMENTS

RESULT 1
US-09-738-626-2884
; Sequence 2884, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MITSUO
; APPLICANT: OCHIAI, KETKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: JP 00/280988
 PRIOR FILING DATE: 2000-08-03
 NUMBER OF SEQ ID NOS: 7059
 SOFTWARE: PatentIn ver. 3.0
 SEQ ID NO 2884
 LENGTH: 1503
 TYPE: DNA
 ORGANISM: Corynebacterium glutamicum
 US-09-738-626-2884

Alignment Scores:

Pred. No.:	1,18e-263	Length:	1503
Score:	2432.00	Matches:	489
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-963-521-2 (1-489) x US-09-738-626-2884 (1-1503)

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QY	21	ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal	40
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QY	41	MetLeuLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp	60
DB	157	ATGAAATTTGGCTGGAGAAATTTGGGATATTTTGTCTTCTTCAGGTACGTCMAATATGAC	216
QY	61	ThrIleValGlnValAlaArgAlaValThrSerAlaArgIleValIleValIleVal	80
DB	217	ACCAAGGTACAAAGTTCAGACAGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	276
QY	81	IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlyValGlyValMet	100
DB	277	ATCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	336
QY	101	AsnValPheHisValAlaGlyValLeuAspThrAsnPheSerIleLeuSerGlyVal	120
DB	337	AACGTTGTTCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	396
QY	121	ArgLeuIleArgSerIleGlnAlaGlyAlaThrProGluValAlaGluValIleLeu	140
DB	397	CGTTGATCCGTTCCATTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	456
QY	141	AspGluLeuGlnIleSerProAlaSerIleGlyPheProValAlaLeuLeuGlyThrAla	160
DB	457	GACGAGTTGGAGCAATCCCTGCGCTTATGCTTTCCTGCTGCTGCTGCTGCTGCTGCT	516
QY	161	MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyIleValIleValIleValIle	180
DB	517	ATGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	576
QY	181	PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyValIleGlyLeu	200
DB	577	TTTATATACCGGTTCCAGATCATTCGACGAGTATTTTGGGAAAGAGGGTTGCT	636
QY	201	ThrPhePheGlnAsnValAlaGlyIlePheIleAlaThrLeuProAlaSerIleAlaThr	220
DB	637	ACTTCTTCCAAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	696
QY	221	SerLeuAlaLeuGlnPheGlyLeuGlnIleValProSerGlnIleIleAlaSerGlyIle	240
DB	697	TCTTTGGCGTTGCAATTTGCTTGAATCAAAACGAGCAAGATCATGCAATCTGAAAT	756
QY	241	ValValIleLeuLeuAlaGlyLeuThrLeuValGlnSerIleGlnAlaGlyIleThrGly	260
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DB	817	CCGCTGACGACGATGACGATTTTTCGAAACCTCTGTTACCGCGCATTTGCT	876
QY	281	GlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuHisValMetLeuProAlaMetGlu	300
DB	877	GGCGTGGTTGGGCAATTCAGCTTTCGAAATCTTGATGATGATGATGATGATGATGAT	936
QY	301	SerAlaAlaAlaProAsnIleSerSerThrPheAlaArgIleIleAlaGlyValThr	320
DB	937	TCCGCTGACGACCTTATTTTCTGCTACATTTGCCCGCATTTATCGTGTGGCTGACC	996
QY	321	AlaAlaAlaPheAlaValAlaGlyCysValAlaGlnIlePheSerValIleAlaGlyLeu	340
DB	997	GACGCGGCTTCCAGAGGTTGTTACGCGAGGTCCTCGGATATTATGGCGGCTT	1056
QY	341	ThrAlaLeuMetGlySerAlaPheThrIleValLeuPheValAlaThrLeuGlyProVal	360
DB	1057	ACTGCGCTGATGGGTTCTGCTTTTATTTACCTCTTCTGTTTATTTAGGCCGCTCT	1116
QY	361	AlaAlaAlaIleAlaThrAlaValAlaGlyPheThrGlyIleLeuAlaArgPhe	380
DB	1117	GCGCTGCGATTTGCTGCAACAGAGTTGTTCACTGCTGCTGCTGCTGCTGCTGCTGCT	1176
QY	381	LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla	400
DB	1177	TTGATTCACCGTTGATTTGCGCATTTGCGGATTCACACCAATGCTTCAGGCTGACA	1236
QY	401	IleThrArgGlyMetThrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle	420
DB	1237	ATTACCGCGAATGATGCGCACCTTAATGATTAACATCACTGATGATTTACCAACAT	1296
QY	421	AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValAlaLeuGlyIleThrIle	440
DB	1297	GCGTTGCTTTAGCATGCTTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1356
QY	441	AlaArgArgLeuArgArgProProArgPheAsnProThrAlaPheThrIleAlaAsn	460
DB	1357	GCCGCGAGGCTACGCTGCTCCACGAGCTTCAACCATACCTGATTTACCAAGCGCAT	1416
QY	461	GluPheSerPheGlnGlnIleAlaGlnIleAsnGlnArgArgGlnIleValArgProIle	480
DB	1417	GAGTTCTCTTCCAGAGAGGAGTGAAGCATACGCGCGAGAGAGAGAGAGAGAGAG	1476
QY	481	ThrAsnGlnArgPheGlyAsnIleArg	489
DB	1477	ACTAATCAGATTCGGTAATTAAGG	1503

RESULT 2
 US-10-627-476-557
 Sequence 557, Application US/10627476
 Publication No. US20040030116A1
 GENERAL INFORMATION:
 APPLICANT: Pompeius, Mark
 APPLICANT: Kroger, Burkhard
 APPLICANT: Schoder, Hartwig
 APPLICANT: Zelder, Oskar
 APPLICANT: Haberhauser, Gregor
 TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT
 TITLE OF INVENTION: TRANSPORT
 FILE REFERENCE: BGI-125PCN
 CURRENT APPLICATION NUMBER: US/10/627,476
 CURRENT FILING DATE: 2003-07-25
 PRIOR APPLICATION NUMBER: 09/602,787
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: USN 60/141031
 PRIOR FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: DE 19931454.3
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931478.0
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931563.9
 PRIOR FILING DATE: 1999-07-08

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; PRIOR APPLICATION NUMBER: DE 1993212.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 1993212.4.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 1993212.5.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 1993212.8.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 557
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXN00349
US-10-627-476-557

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Alignment Scores:

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Pred. No.:      1,296-263      Length:      1590
Score:          2432.00      Matches:      489
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               13          Gaps:          0

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US-09-963-521-2 (1-489) x US-10-627-476-557 (1-1590)

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QY      1 MetIeuSerPheAlaThrIeuAraGlyArgIleSerThrValAspAlaIalysalaa 20
DB      101 ATGTTAGATTTCGCGACCTTCGTGGCCGCAATTTCACAGTTGACCTGCAAAAGCCGGA 160

QY      21 ProProSerProleuAlaProIleAmpIeuThraSphSerGluValaIaglyVal 40
DB      161 CCTCCGCCATCGCCACTAGCCCGGATTGATCTCAAGCAATGTAAGTGGCGGTGTG 220

QY      41 MetAsnIeuAlaIalArgIleGlyAspIleIeuIeuSerSerGlyThrSerAsnSerAsp 60
DB      221 ATGAATTTGGCTGCGGAATTTGGCGAATTTTGGCTTCTTCAGTACGTCGAATAGTGAC 280

QY      61 ThrIysValGluValaIArgAlaValThrSerAlaTyrglyIeuTyrrThrHisValaAsp 80
DB      281 ACCAAGATCAAGATTGAGACAGTGAACCTCTGGGTGTAAGTTGATACACGACGCGGAT 340

QY      81 IleThrIeuAsnThrIleThrIlePheThrAsnIleGlyValGluArgIysMetProVal 100
DB      341 ATCAAGTTGAATACGATCAACATCTTCACCAACATCGGTGTGAGAGGAATGCCGCGTC 400

QY      101 AsnValaIleHisValaIalGlyIeuAspThrAsnPheSerIysIeuSerGluValaAsp 120
DB      401 AACGATTTCAATGTTGTAGGCAAGTTGGACACCAATTTCTCCAACTGCTTGAGGTTGAC 460

QY      121 ArgIeuIleArgSerIleGluAlaGlyAlaThrProProGluValaIaGluIysIleIeu 140
DB      461 CGTTTGATCCGTTCAATCAAGCTGTGTGCGACCCGCGTGAAGTGGCCGAGAAATCTCG 520

QY      141 AspGluIeuGluIeuSerProIaSerTyrglyPheProValAlaIeuIeuIyrrPala 160
DB      521 GACGAGTTGAGCAATCCCTCGCTTATAGGTTTCCCTGTGCGGTGTGCTGGCGGA 580

QY      161 MetMetGlyIalValaIalValaIeuIeuGlyIyrrGluValaSerIeuIleAla 180
DB      581 ATGATGGGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 640

QY      181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheIeuGlyIysIysGlyIeuPro 200
DB      641 TTATATACCGGCTTACATCAATTCACGACGATATTTTGGGAAAGAGGTTTGCT 700

QY      201 ThrPheGluIeuAsnValaIalGlyIlePheIleAlaThrIeuProIaSerIleAlaTyrr 220

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DB      701 ACTTCTTCCAAATGTTGTGGTATTATGCGACGCTGCTGATGATTCCTAT 760
QY      221 SerIeuAlaIeuGluIlePheGlyIeuGluIleIysProSerGluIleIleAlaSerGlyIle 240
DB      761 TCTTTGGCGTTGAATTTGTTGTTGATCAAAACCGGACGATCAATCGCATCTGGAAAT 820
QY      241 ValValIeuIeuAlaGlyIeuThrIeuValaIaSerIeuGluIleIleIleIleValaIa 260
DB      821 GTTGTGCTGTGGCAGGTTTGAACCTGTCATTTCTGCAAGACGCGCATCAAGGCGCT 880
QY      261 ProValThrAlaSerAlaArgPhePheGluThrIeuIeuPheThrGlyIyrrIleValaIa 280
DB      881 CCGGTACAGCAGATGACGATTTTCAAAACCTCGTTTACCGGCGGCAATTTGCT 940
QY      281 GlyValGlyIeuGlyIleGluIeuSerGluIleIleHisValaMetIeuProIaIleGlu 300
DB      941 GCGGTGGGTTGGGCAATTCAGCTTTCGAATCTTCATGTCAATGCTGCTGCTGCTGAG 1000
QY      301 SerAlaAlaIalProAsnTyrrSerSerThrPheAlaArgIleIleIleIleIleValaIa 320
DB      1001 TCCGCTGACGACCTTAATTTATTTGCTACATTTGCGCCGCAATTCGCTGAGGCGTACC 1060
QY      321 AlaAlaIalPheAlaValaIalGlyTyrrAlaIalIyrrPheSerValIleIleIleIleIle 340
DB      1061 GCAGCGGCTTCGCAATGGGTTGTACGCGAGTGTCTCGGTATTTATTCGGGGCTT 1120
QY      341 ThrAlaIeuMetGlySerAlaPheTyrrTyrrIeuPheValaIalTyrrIeuGlyProValSer 360
DB      1121 ACTGCGCTAATGGGTTGTGGTTTATTAACCTCTTGTGTTTATTTAGGCCCCGCTCTCT 1180
QY      361 AlaAlaAlaIleAlaIalThrAlaValaIalGlyPheThrGlyIyrrIeuIeuAlaArgPhe 380
DB      1181 GCGCGTGGATTCCTGCAACAGAGTGTTCACGCGGTGTTGCTTCCCGCTGATTC 1240
QY      381 IeuIleProProIeuIleValaIalIleIleIleIleIleIleIleIleIleIleIleIle 400
DB      1241 TTGATTCACCGCTGATTTGGCGATTCGCGCATCACACCAATGCTTCAGGTCTAGCA 1300
QY      401 IleTyrrArgGlyMetTyrrAlaThrIeuAsnAspGluIleIeuMetGlyPheThrAsnIle 420
DB      1301 ATTTCAGGGAATGACCCACCTCGAATGATCAACACTAGGAGTTTCACCAACAT 1360
QY      421 AlaValaIalIleAlaIalThrAlaSerSerIeuAlaIalGlyValaIleIleIleIleIle 440
DB      1361 GCGGTGCTTTAGCCACATGCTTCATCACTTGGCGGTGTTGTTGTTGTTGTTGTTGTTGTT 1420
QY      441 AlaArgIleIeuIleArgProProIalArgPheAsnProTyrrAlaIalPheThrIysAlaAsn 460
DB      1421 GCCCGAGGCTTACGTGCTCCACACGCTTCAACCATACCGTCAATTTACCAAGCGGAAT 1480
QY      461 GluPheSerPheGluIleGluIleIleIleIleIleIleIleIleIleIleIleIleIle 480
DB      1481 GAGTTCTCTTCCAGAGAGAGCTGACGAATACAGCGCGGCAAGAAAGCTCCAAAG 1540
QY      481 ThrAsnGluIleArgPheGlyAsnIysArg 489
DB      1541 ACTAATCAGAGATTCGTTATTAAGG 1567

RESULT 3
US-10-450-055-41
; Sequence 41, Application US/10450055
; Publication No. US20040043953A1
; GENERAL INFORMATION:
; APPLICANT: BASF Aktiengesellschaft
; TITLE OF INVENTION: No. US20040043953A1el genes of Corynebacterium
; FILE REFERENCE: 936 2000
; CURRENT APPLICATION NUMBER: US/10/450, 055
; CURRENT FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 41
; LENGTH: 1590

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TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1567)
OTHER INFORMATION: RXS00349
US-10-450-055-41

Alignment Scores:
Pred. No.: 1,296-263 Length: 1590
Score: 2432.00 Matches: 489
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-963-521-2 (1-489) x US-10-450-055-41 (1-1590)

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QY 1 MetLeuSerPheAlaThrLeuAArgIleSerThrValAspAlaAlaAla 20
DB 101 ATGTTGAGTTTTCGACCCCTTCGTGGCCGCAATTTCACAGTTGACGCTGCAAAAGCCGCA 160
QY 21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
DB 161 CCTCCGCCATGCGCAGTACGCCGATGATCTCACTGACCAATAGTCAAGTGGCCGCTGTG 220
QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerGlyThrSerAsnSerAsp 60
DB 221 ATGAAATTTGGCTGGGAATATGGCGATATTTGCTTCTTCAGGTACGTCAAATAGTGAC 280
QY 61 ThrIleValGlnValAlaArgAlaValThrSerAlaArgIleuValThrHisValAsp 80
DB 281 ACCAAGGTACAGATTCAGAGAGTGCACCTTCGCTGACGATTTGACTACAGCAGCTGAT 340
QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGluArgGlyMetProVal 100
DB 341 ATCAAGTTGAATAGATACCATCTTCAACCAATCGGTGGAGAGGAATCCGCTC 400
QY 101 AsnValPheHisValAlaGlyIleLeuAspThrAsnPheSerIleLeuSerGluValAsp 120
DB 401 AACCTGTTTCAATGTTGAGGCAAGTGGACACCAACTTCCAAACTGTCTGAGAGTTGAC 460
QY 121 ArgLeuIleAspSerIleGlnAlaGlyAlaThrProProGluValAlaGluIleLeu 140
DB 461 CGTTTGATCCCTTCATTCAGCTGCGTGGCGACCCCGCTGAGGTTGCCGAGAAATCTGT 520
QY 141 AspGluLeuGluGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrAla 160
DB 521 GACGAGTTGGAGCAATCCCTGCGCTTATGCTTCCCTGTTGCTGCTGGCTGGCA 580
QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyIleTyrGlnValSerLeuIleAla 180
DB 581 ATGATGGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640
QY 181 PheIleThrAlaPheThrIleIleIleAlaThrIleSerPheLeuGlyIleValGlyLeuPro 200
DB 641 TTTATACCGGCTTCACATCATTCGACGAGTATTTTGGAGAAAGAGGTTGCT 700
QY 201 ThrPhePheGlnAsnValAlaGlyIlePheIleAlaThrLeuProAlaSerIleAlaTyr 220
DB 701 ACTTTCTTCCAAATGTTGTTGCTGCTGCTTATATGCAAGCTGCTGCTGCTGCTGCTGCT 760
QY 221 SerLeuAlaLeuGlnPheGlyLeuGluIleLysProSerGlnIleIleAlaSerGlyIle 240
DB 761 TCTTTGGGCTTCGCAATTTGCTTGAATCAAAACGAGCAGATCATGCACTCTGAAAT 820
QY 241 ValValIleLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260
DB 821 GTTGGCTGCTGGCGAGTTTGAACCTCGGCAATCTGCGAGGAGCGCATCAGGCGCT 880
QY 261 ProValThrAlaSerAlaArgPhePheGluThrLeuLeuPheThrGlyIleValAla 280
DB 881 CCGGAGACGACGAGGAGGATTTTCCAAACACTCCTGTTTACCGGCGGCAATGTTGCT 940
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QY 281 GlyValGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu 300
DB 941 GCGGTGGTTTGGGCAATTCAGCTTCTGAAATCTTCAGATCTCATGTTCCCTGCGCATGGAG 1000
QY 301 SerAlaAlaAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyValAlaThr 320
DB 1001 TCCGCTGACGACCTTAATATTCGTCTACATTCGCCGCGATTCGCTGCTGCTGCTGCTGCT 1060
QY 321 AlaAlaAlaPheAlaValAlaGlyCysIleValAlaGluTyrSerSerValIleIleAlaGlyLeu 340
DB 1061 GCAGCGGCTTCGCAAGTGGGTTGTACGCGAGTGTCTCGGATGATTAATTCGCGGCTT 1120
QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValAlaTyrLeuGlyProValSer 360
DB 1121 ACTGCGTGAAGGCTTCGCTGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1180
QY 361 AlaAlaAlaIleAlaAlaThrAlaValAlaGlyPheThrGlyIleLeuAlaAlaArgPhe 380
DB 1181 GCGGCTGCGATTCGTCGCAACGAGTTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240
QY 381 LeuIleProProLeuIleValAlaAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
DB 1241 TTGATTCACCGTTGATTTGGCGATTCGCGCATCAACCAATGCTTCCAGGCTAGCA 1300
QY 401 IleTyrArgIleMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
DB 1301 ATTTACCGCGAATGTAAGCCCACTTGAATCAATCAATCAATCAATCAATCAATCAATCAAT 1360
QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyIleTyrIle 440
DB 1361 GCGGTTGCTTACGACATGCTTCATCACTTCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420
QY 441 AlaArgArgLeuArgArgProProArgPheAsnProTyrArgAlaPheThrIleAlaAsn 460
DB 1421 GCCGCGAGGCTACGCTTCACCAAGCTTCACCAAGCTTCACCAAGCTTCACCAAGCTTCAC 1480
QY 461 GluPheSerPheGlnGlnGluAlaGlyIleAsnGlnArgArgGlnArgIleArgProIle 480
DB 1481 GAGTTCTCTTCCAGGAGGAAGTGCAGACAGATAGCGCGCGAGAGAGAGAGAGAGAGAGAG 1540
QY 481 ThrAsnGlnArgPheGlyAsnLysArg 489
DB 1541 ACTAATCAGAGATTCGGTAATAAAGG 1567
```

RESULT 4
US-09-951-536-3
Sequence 3, Application US/09951536
Patent No. US20020107378A1
GENERAL INFORMATION:
APPLICANT: ZIEGLER, PETRA
APPLICANT: EGGELENG, IOTHAAR
APPLICANT: SAHM, HERMANN
APPLICANT: THIERBACH, GEORG
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
FILE REFERENCE: 21123/282414/MAS
CURRENT APPLICATION NUMBER: US/09/951,536
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/431,099
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1909
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (280)..(1746)
OTHER INFORMATION: tnfE-Gen
US-09-951-536-3

Alignment Scores:

Pred. No.: 1,71e-263 Length: 1909
 Score: 2432.00 Matches: 489
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-963-521-2 (1-489) x US-09-951-536-3 (1-1909)

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QY 1 MetLeuSerPheAlaThrLeuArgGlyArgIleSerThrValAspAlaIleValAla 20
DB 280 ATGTTGATTTTGGACCCCTTCGTCGCGCATTTCAACAGTTGACCGTGAAGCCGCGCA 339
QY 21 ProProPheSerProLeuAlaProIleAspLeuThrAspHisSergIleValAla 40
DB 340 CCGCCGCGCATCGCACATGACCCCGATTTGATCTCACTGACCATAGTCAGAGCCCGGTTG 399
QY 41 MetAsnLeuAlaIleArgIleGlyAspIleLeuLeuSerSergIlyThrSerAsnSerAsp 60
DB 400 ATCAATTTGGCTGCGGAATTTGGCATATTTGCTTCTTCAGGTACGTCAATAGTGAC 459
QY 61 ThrIleValGlnValArgAlaValThrSerAlaTyrGlyLeuTyrTyrThrHisValAsp 80
DB 460 ACCAAGGTACAGATTGACAGACGTGACCTTCGCTACGAGTTTGATCAACGACGCGTGAT 519
QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgIlyMetProVal 100
DB 520 ATCAGCTGAAATGACATGACATCCATCTTCAACCAATCGGTGTGAGAGAGAGATGCGGTC 579
QY 101 AsnValPheHisValValGlyIlyLeuAspThrAsnPheSeriIySleuSergIlyValAsp 120
DB 580 AACGTGTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTGAGGTTGAC 639
QY 121 ArgLeuIleArgSeriIleGlnAlaGlyAlaThrProProGlnValAlaGlnIlySleu 140
DB 640 CGTTTGATCCGTTCCATTGAGGTGAGTGGACCCCGCCGAGGTTGCCAGAAATCCCG 699
QY 141 AspGlnLeuGlnIleSerProAlaSerIyGlyPheProValAlaLeuLeuGlyTyrPala 160
DB 700 GACGAGTTGGACGACATCCCTCGCTTATGTTTCCCTGTCGTTGCTTGCGTGGGCA 759
QY 161 MetMetGlyAlaValAlaValLeuLeuGlyIlyTyrGlnValSerLeuIleAla 180
DB 760 ATGATGGGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 819
QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIlySleuSergIlyPro 200
DB 820 TTATATTCGCGCTTCACATGATGACGACGACGATCAATTTTGGAAAGAGGTTTGCT 879
QY 201 ThrPhePheGlnAsnValValGlyIlyPheIleAlaThrLeuProAlaSerIleAlaTyr 220
DB 880 ACTTCTTCGAAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 939
QY 221 SerLeuAlaLeuGlnPheGlyLeuGlnIleIyProSergIleIleAlaSerGlyIle 240
DB 940 TCTTGGCGGTGCAATTTGGTCTTGAAGTCAAAACCGAGCGACATGATCATCTGGAATT 999
QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260
DB 1000 GTTGTGCTGTGGACGTTTGACATCTGTCGCAATCTTGGACGAGGACGTCACGCGGCT 1059
QY 261 ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIlyIleValAla 280
DB 1060 CCGGTCAGACGACGACGACGATTTTTCGAAACACTCCGTTTACCGGGGCGGATTTTGCT 1119
QY 281 GlyValGlyLeuGlyIlyLeuLeuSergIlyIleLeuHisValMetLeuProAlaMetGln 300
DB 1120 GCGGTGGGTTGGGATTCAGCTTCTTGAATCTTGACATGTCATTTGCTGCGCATGAG 1179
QY 301 SerAlaAlaAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyValThr 320

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DB 1180 TCGCTGACAGACCTAATTATTCGTACATTCGCCCGCATTAATCGGTGCGTACCC 1239
QY 321 AlaAlaAlaPheAlaValGlyCysTyrAlaGlnThrSerSerValIleIleAlaGlyLeu 340
DB 1240 GCAAGGCTTCGTCAGATGGGTGTACGCGAGGTGTCTCGGTATTAATTTGGCGGCTT 1299
QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProValSer 360
DB 1300 ACTGCGCTGATGGGTTCTGCTTTTATTAATCTTCTGCTTGTATTTAGGCCCGCTCT 1359
QY 361 AlaAlaAlaIleAlaAlaThrAlaValAlaGlyPheThrGlyIlyLeuLeuAlaArgPhe 380
DB 1360 GCCGTCGACATTCGTCACACAGACGATGTTTCACTGATGATGATGATGATGATGAT 1419
QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
DB 1420 TTGATTCACCGTTGATTTGTGGATTTGCCGATCAACCAATGCTTCCAGGTCTAGCA 1479
QY 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
DB 1480 ATTACCGGGAATGATACGCCACCTGATGATCAACAATCTGATGATGATGATGATGAT 1539
QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaIleGlyValValLeuGlyIlyTyrPala 440
DB 1540 GCGGTGCTTTAGCCATGCTTCATCATCACTTGCCTGCGGTGGTTGGTGGTGGAT 1599
QY 441 AlaArgIleLeuArgProProArgPheAsnProTyrArgAlaPheThrIlySalaAsn 460
DB 1600 GCCCGAGGCTACGTGTCCACGACGCTTCAACCCATACCGTACATTCACCAAGGGAAT 1659
QY 461 GluPheSerPheGlnGlnGlnAlaGlnIleAsnGlnArgArgGlnArgIlySargProIly 480
DB 1660 GAGTTCTCTTCCAGAGAGAACTGACGAGAAATCAGGCGCGGAGAGAAAGCTCCAAAG 1719
QY 481 ThrAsnGlnArgPheGlyAsnIlySarg 489
DB 1720 ACTAATCAGAGATTCGTTAATAAAG 1746

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RESULT 5

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US-09-963-521-3
Sequence 3, Application US/09963521
Patent No. US20020146781A1
GENERAL INFORMATION:
APPLICANT: ZIEGLER, PETRA
APPLICANT: EGGELING, LOTHAR
APPLICANT: SAHM, HERMANN
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE
TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
FILE REFERENCE: 21123/282413/MAS
CURRENT APPLICATION NUMBER: US/09/963,521
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/431,099
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: DE 199 41 478.5
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1909
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (280)..(1746)
OTHER INFORMATION: thrE-gen
US-09-963-521-3

```

Alignment Scores:
 Pred. No.: 1,71e-263 Length: 1909
 Score: 2432.00 Matches: 489
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-963-521-2 (1-489) x US-09-963-521-3 (1-1909)

```

QY 1 MetLeuSerPheAlaThrLeuArgGlyYArgGlyLeSerThrValAlaAlaValAla 20
DB 280 ATGTTGAAGTTTGGCAACCTTCGTGGCCGCAATTCACAGTTACCGCTGCAAAAGCCGCA 339
QY 21 ProProPseSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
DB 340 CCCCCCGCATCGCACAATGCGCCGATTTGATCTCAGCAGCATAGTCAGAGGCGCGGTGTC 399
QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
DB 400 ATGAATTTGGCTCGAGAAATGGCGAATTTGCTTCTTCAGGTACGTCAAAATAGTGAC 459
QY 61 ThrIleValGlnValAlaThrAlaValThrSerAlaTyGlyLeuTyThrHisValAsp 80
DB 460 ACCAAGGTACAGATTGAGAGGACCTCTGCGTACGGTTTGTACTACACGACGTGGAT 519
QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgIleMetProVal 100
DB 520 ATCAGCTTGAATGACATCACCATTCTCACCACATCGGTGGAGAGAGATGCCGCTC 579
QY 101 AsnValPheHisValValGlyIleLeuAspThrAsnPheSerIleLeuSerGlnValAsp 120
DB 580 AACGTTTTCATGTTGAGGCAAGTTGGACACCAACTTCTCCAAACTGCTGAGGTGAC 639
QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGlnValAlaGlnIleLeu 140
DB 640 CGTTTGATCCGTTTCATTCAGGCTGGTGCGAACCCGCGCTGAGTTGCCGAGAAATCCTG 699
QY 141 AspGlnLeuGlnGlnSerProAlaSerTyGlyPheProValAlaLeuLeuGlyTyPAla 160
DB 700 GACGAGTTGAGGACATCCCTGCGCTTATGTTTCCCTGTTGCTTGGCTGGCGCA 759
QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyTyPProGlnValSerIleAla 180
DB 760 ATGATGGGTGGTGTGTTGCTGTGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 819
QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIleTySlyGlyLeuPro 200
DB 820 TTTATTCACGGGTTTACGATCATTTGCCACGACGTCATTTTGGGAAAGAGGTTTGCT 879
QY 201 ThrPhePheGlnAsnValAlaGlyIlePheIleAlaThrLeuProAlaSerIleAlaTy 220
DB 880 ACTTCTTCCAAATGTTGTGTGTGTATTTATGCCACGCTGCTGCATCGATTGCTTAT 939
QY 221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLeysProSerGlnIleIleAlaSerGlyIle 240
DB 940 TCTTTGGCGTTGCAATTTGCTTGAGTCAACCGACCGACGATCGCATCTGGAAATT 999
QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260
DB 1000 GTTGTGCTGTGGAGGTTTGACCTGTGCATCTTGACGAGCGGATCACGGGCGCT 1059
QY 261 ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIleValAla 280
DB 1060 CCGGTGACAGCAAGTGACGATTTTTCGAAACACTCTGTTTACCGGGCGGATGTTGCT 1119
QY 281 GlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuHisValMetLeuProAlaMetGlu 300
DB 1120 GCGGTGGGTGGGATTCAGCTTCTTAATCTTGCAATCTTGCAATCTTGCCCTGCCATGAG 1179
QY 301 SerAlaAlaAlaProAsnTySerSerThrPheAlaArgIleIleAlaGlyValThr 320
DB 1180 TCCGCTGAGACACCTAATTTATTCCTACATTCGCCCGCATTTATCGTGAGCGCTCAC 1239
QY 321 AlaAlaAlaPheAlaValAlaGlyCysTyAlaGlnTyPserSerValIleIleAlaGlyLeu 340
DB 1240 GCAGCGGCTTCGAGTGGTGTGTACCGGAGTGCTCGGTGATTAATTTGCGGGGCTT 1299

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QY 341 ThrAlaLeuMetGlySerAlaPheTyTyLeuPheValValTyLeuGlyProValSer 360
DB 1300 ACTGCGCTATGGGTTCTCGCGTTTATTAACCTTCTGTTGTTATTTAGGCCCGCTCTCT 1359
QY 361 AlaAlaAlaIleAlaAlaThrAlaValGlyPheThrGlyIleLeuLeuAlaArgPhe 380
DB 1360 GCGGTGACGATTCGTCAACAGCAGATGGTTTCACAGGTGGTGTGCTGGCCGTCATTC 1419
QY 381 LeuIleProProLeuIleValAlaAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
DB 1420 TTGATTCACCGTTGATGATGGGATTTGGCGATTCGCGATACACCAATGCTTCCAGSTCTAGCA 1479
QY 401 IleTyArgGlyMetTyAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
DB 1480 ATTTCACGGGATGATGACGCACTCGAATGATCAACAACCTAGGTTTACCAACAATT 1539
QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyIleTyPle 440
DB 1540 GCGGTGCTTTTACCCACTGCTCATCATCTGCGCTGGCTGGTGGTGGTGGTGGTGGT 1599
QY 441 AlaArgArgLeuArgArgProProArgPheAsnProTyArgAlaPheThrIleAlaAsn 460
DB 1600 GCCCGAGGCTACGATGCTCCACACCGCTTCAACCATTCCTGATTTACCAAGCGCAT 1659
QY 461 GluPheSerPheGlnGlnGlnAlaGlnGlnAsnGlnArgArgGlnArgIleTySlyProlys 480
DB 1660 GAGTTCTCTTCCAGAGGAACTGAGCAGATCAGCGCGGAGAGAGAGAGAGAGAGAGAG 1719
QY 481 ThrAsnGlnArgPheGlyAsnIleTySlyArg 489
DB 1720 ACTAATCAGAGATTCGTTAATAAAAG 1746

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RESULT 6
US-09-834-721-3
Sequence 3, Application US/09834721
Patent No. US2002015551A1
GENERAL INFORMATION:
APPLICANT: RIEBING, MECHTHILD
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
FILE REFERENCE: 21132/280169/MAS
CURRENT APPLICATION NUMBER: US/09/834,721
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: DE 100 26 494.8
PRIOR FILING DATE: 2000-05-27
PRIOR APPLICATION NUMBER: DE 101 02 823.7
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentm Ver. 2.1
SEQ ID NO 3
LENGTH: 1909
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURES:
OTHER INFORMATION: ATCC13032
NAME/KEY: CDS
LOCATION: (280)..(1746)
OTHER INFORMATION: thre gene
US-09-834-721-3

Alignment Scores:
Pred. No.: 1.71e-263 Length: 1909
Score: 2432.00 Matches: 489
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-963-521-2 (1-489) x US-09-834-721-3 (1-1909)

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QY 1 MetLeuSerPheAlaThrLeuArgGlyYArgGlyLeSerThrValAlaAlaValAla 20
DB 280 ATGTTGAAGTTTGGCAACCTTCGTGGCCGCAATTCACAGTTACCGCTGCAAAAGCCGCA 339

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QY 21 ProProSerProLeuAlaProIleAspLeuThrAspHisSerGluValAlaGlyVal 40
 Db 340 CTTCCGCGCATTCGACATTCAGCCCATGATTCCTCACTGACATTAATCAAGTGGCGGCTG 399
 QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
 Db 400 ATGAATTTGGCTGGCGAATTGGCGAATTTTGGCTTCTTCAGGTACGTAAATATGATGAC 459
 QY 61 ThrIleValGlnValAlaGlnAlaValThrSerAlaTyrlGlyLeuTyrlThrHisValAsp 80
 Db 460 ACCAAGGTACAGATTCAGAGAGTGAACCTTCGCTGACGTTGTACTACAGCGACGTGGAT 519
 QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGluGlySerMetProVal 100
 Db 520 ATACGTTGATATGATGATACCATTCATTCACCAATCGGTGTGAGAGAGATGCCGCTC 579
 QY 101 AsnValPheHisValValGlyLysLeuAspThrAsnPheSerLysLeuSerGluValAsp 120
 Db 580 AACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGAC 639
 QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGluLysIleLeu 140
 Db 640 CGTTTATCCGTTCCATTCAGCGTGGCGACCCCGCTGAGGTTGCCAGAAATCTCTG 699
 QY 141 AspGluLeuGluGlnSerProAlaSerTyrlGlyPheProValAlaLeuLeuGlyTyrlAla 160
 Db 700 GACGATTTGGAGAAATCCCTGCGCTTATAGTGTTCCTGCTGCTGCTGCTGCTGCTGCT 759
 QY 161 MetMetGlyValAlaValAlaValLeuLeuGlyGlyValTyrlPheValSerLeuIleAla 180
 Db 760 ATGATGGTGGTGGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 819
 QY 181 PheIleThrAlaPheThrIleIleAlaAlaThrThrSerPheLeuGlyLysIleGlyLeuPro 200
 Db 820 TTTATTAACCGCTTCACGATTCATTCGACGACGCTCATTTTGGGAAGAAGGTTGGCT 879
 QY 201 ThrPhePheGlnAsnValValGlyLysPheIleAlaThrLeuProAlaSerIleAlaTyrl 220
 Db 880 ACTTTCCTCCAAATGTTGTGTGTTGTTATTTATGCGACGCTGCTGCATTCGATTCCT 939
 QY 221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLysProSerGlnIleIleAlaSerGlyIle 240
 Db 940 TCTTTGGCGTTGCAATTTGGTCTTGAGATCAACCGACGACATTCGATTCGTAAT 999
 QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260
 Db 1000 GTTGGCTGTTGGCAGGTTTGACACTCGGCAATCTCTCGACGACGCGGCTGCT 1059
 QY 261 ProValThrAlaSerAlaPhePheGlyThrLeuLeuPheThrGlyGlyIleValAla 280
 Db 1060 CCGGTGACGACAGTGCAGATTTTTCGAAACACTTCCTGTTTACCGCGCGCATTTGTTGCT 1119
 QY 281 GlyValGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu 300
 Db 1120 GCGGTGGGTTTGGCATTCAGCTTCTGAAATCTTGACATGTCATGTTGCTGCCATGAG 1179
 QY 301 SerAlaAlaAlaProAsnTyrlSerSerThrPheAlaArgIleIleAlaGlyValThr 320
 Db 1180 TCCGCTGACGACCTTAATTAATTCGTCATTCGCGCGCATTAATGCTGTGGCTGAC 1239
 QY 321 AlaAlaAlaPheAlaValGlyCysTyrlAlaGluTyrlPheSerValIleIleAlaGlyLeu 340
 Db 1240 GCAAGGCGCTTCGACGTGGGTTGTTACCGGAGAGTGTCTCGGTATTAATGGCGGCT 1299
 QY 341 ThrAlaLeuMetGlySerAlaPheTyrlTyrlLeuPheValAlaTyrlLeuGlyProValSer 360
 Db 1300 ACTGGCTGATGGGTTCTGCGTTTATTAACCTTCGTTGTTTATTAAGCCCGCTCTCT 1359
 QY 361 AlaAlaAlaIleAlaAlaThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgArgPhe 380
 Db 1360 GCGGCTGGATTTGCGCAACGACAGTGTGTTACCTGAGGTTTGCCTTCCCGCTGATTC 1419
 QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400

Db 1420 TTGATTCACCGTGTGATTTGGGAGATTCGCGCATCACAACCAATGCTTCCAGGCTGAC 1479
 QY 401 IleTyrlArgIleGlyMetTyrlAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
 Db 1480 ATTTACCGCGGAATGTAGCGCACCTCGAATGATCAACAACCTCATGAGGTTTCCACCAAT 1539
 QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValAlaLeuGlyGluTyrlIle 440
 Db 1540 GCGGTGCTTTACCGACTGCTTCACTCACTTCGCGCTGGCTGGTTTGGGTGAGTGAT 1599
 QY 441 AlaArgArgLeuArgArgProProArgPheAsnProTyrlArgAlaPheThrLysAlaAsn 460
 Db 1600 GCCCGAGGCTACGTCGTCACACAGCTTCAACCCATACCGTGATTTACCAAGCGCAAT 1659
 QY 461 GluPheSerPheGlnGlnGluAlaGluGlnAsnGlnArgArgGlnArgGlySerProLys 480
 Db 1660 GAGTTCTCTTCCAGAGAGAACTGAGCAAAATCAGCGCGGAGAGAAAAAGTCCAAAG 1719
 QY 481 ThrAsnGlnArgPheGlyAsnLysArg 489
 Db 1720 ACTAATCAGAGATTCGCTAATTAAGG 1746

RESULT 7
 US-09-783-388-3
 ; Sequence 3, Application US/09783388
 ; Patent No. US20020168731A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ziegler, Petra
 ; APPLICANT: Eggeling, Lothar
 ; APPLICANT: Sahm, Hermann
 ; APPLICANT: Thierbach, Georg
 ; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
 ; TITLE OF INVENTION: PROCESS FOR
 ; FILE REFERENCE: 21123/27066
 ; CURRENT APPLICATION NUMBER: US/09/783,388
 ; CURRENT FILING DATE: 2001-02-15
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 1909
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum ATCC13032
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (280)..(1746)
 US-09-783-388-3

Alignment Scores:
 Pred. No.: 1,71e-263 Length: 1909
 Score: 2432.00 Matches: 489
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-963-521-2 (1-489) x US-09-783-388-3 (1-1909)

QY 1 MetLeuSerPheAlaThrLeuArgGlyArgIleSerThrValAspAlaAlaLysAlaAla 20
 Db 280 ATGTTGAGATTTTGGCAACCTTCGTGGCGCATTTCAACAGTTGACGCTGCACAAAGCGCGA 339
 QY 21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGluValAlaGlyVal 40
 Db 340 CTTCCGCGCATTCGACATTCAGCCCATGATTCCTCACTGACATTAATCAAGTGGCGGCTG 399
 QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
 Db 400 ATGAATTTGGCTGGCGAATTGGCGAATTTTGGCTTCTTCAGGTACGTAAATATGATGAC 459
 QY 61 ThrIleValGlnValAlaGlnAlaValThrSerAlaTyrlGlyLeuTyrlThrHisValAsp 80

Db 460 ACCAAGGTAAGAATTGACAGTACCTCTGCGTACGCTTTGACTACACGACCTGGAT 519
 QY 111ethrLeuAsnThr11ethr11ephethrAsn11eglyVal1GluArg1ysMetProVal 100
 Db 520 ATCACTTGAATACGATACACATCTTACCAACATCGGTGTGAGAGAAATGCGGCTC 579
 QY 101 AenValPheHisValVal1Gly1sLeuAspThrAsnPheser1ysLeuSerGlyValAsp 120
 Db 580 AACGCTTCATCTTGTAGGCAAGTGGACACCACTTCTCCAACTGCTGAGGTTGAG 639
 QY 121 ArgLeu11leuSer11egln1aGlyVal1aThrProProGluVal1aGlu1ys1leu 140
 Db 640 CGTTTGATCCGTTCCATTACGCTGCGGCACTCCGCGCTGAGGTTGCCGAAATCTCTG 699
 QY 141 AspGluLeuGluGlnSerProAlaSerTyrGlyPheProVal1aLeuLeuGly1TTPAla 160
 Db 700 GACGAGTTGAGCAATCCCTGCGCTTATGATTCCTGCTGCTGCTGCTGCTGCTGCTG 759
 QY 161 MetMetGlyGlyValVal1aVal1LeuLeuGlyGly1TTPGlnVal1SerLeu11a1a 180
 Db 760 ATGATGGGTGGT 819
 QY 181 Phe11ethr1aPheThr11le1a1aThr1aSerPheLeuGly1ys1sGlyLeuPro 200
 Db 820 TTTATTTACCGCTTACGATCATTTGCCACGACGATTTTGGGAAAGGAGGTTGCTT 879
 QY 201 ThrPhePheGlnAsnValVal1Gly1Phe11a1aThr1eupProAlaSer11a1aTyr 220
 Db 880 ACTTCTTCCAAATGTTGT 939
 QY 221 SerLeu1aLeuGlnPheGlyLeuGln11elyProSerGln11e11a1aSerGly1le 240
 Db 940 TCTTTGGCGTTGAATTTGCTTGAATCAACCGACGATCATGCACTGCGAATT 999
 QY 241 ValVal1LeuLeu1aGlyLeuThrLeuValGlnSerLeuGlnAspGly11ethrGlyVala 260
 Db 1000 GTTGTGCTGTTGCGAGGTTTGACCTGTGCACTCTGCGACGCGGATCACGGCGCT 1059
 QY 261 ProValThr1aSer1aArgPhePheGluThrLeuLeuPheThrGly11eVal1a1a 280
 Db 1060 CCGGTGACAGCAAGTGCAGATTTTTCGAAACACTCCGCTTACCGCGGCGATTTGCT 1119
 QY 281 GlyVal1GlyLeuGly11eglnLeuSerGlu11eLeuHisVal1MetLeuProAlaMetGlu 300
 Db 1120 GCGGTGGGTTTGGGATTCACCTTGTGAATCTTGCAATGTCATGTTGCTCGCATGGAG 1179
 QY 301 Ser1a1a1a1aProAsnTyrSerSerThrPhe1aArg11e1a1aGly1Val1aThr 320
 Db 1180 TCCGCTGACGACCTTAATTTGCTTACATTCGCGCGCATTTATGCGTGGGCGTCAAC 1239
 QY 321 Ala1a1a1aPhe1a1aVal1GlyCysTyr1aGlu1TTPSerSerVal11e1a1aGlyLeu 340
 Db 1240 GCAAGGCGCTTCGCGAGGTTGTTCACCGGAGTGTCTCGGTGATTAATTCGCGGCTT 1299
 QY 341 Thr1a1a1eumMetGlySer1a1aPheTyr1eupPheVal1Val1TyrLeuGly1ProValSer 360
 Db 1300 ACTGGGTGATGAGGTTTGGCTTTATTAACCTTCTGTTGTTATTTAGGCCCTCTCT 1359
 QY 361 Ala1a1a1a1a1a1a1a1a1aVal1GlyPheThrGly1GlyLeuLeu1a1aArg1Phe 380
 Db 1360 GCCGCTGCGATTTGCGAACAGCAAGTGGTTTCACTGGGTTGCTTGGCGCTGATTC 1419
 QY 381 Leu11eProProLeu11eVal1a11e1a1aGly11eThrProMetLeuProGly1eVala 400
 Db 1420 TTGATTTCCACCGTTATTTGTGCGATTCGCGCATCACCAATGCTTCAGGCTCAGGA 1479
 QY 401 11elyr1a1sGly1ysMetTyr1a1aThr1euaAspGlnThrLeuMetGly1PheThrAsn1le 420
 Db 1480 ATTATCCGGGGAATGACCACTCGATGATCAACAACCTCATGGGTTTACCAACAT 1539
 QY 421 AlaVal1a1a1eVal1a1a1a1a1a1a1a1a1a1aGly1Val1a1eGly1e1u1TTP1le 440
 Db 1540 GGGGTGCTTTAGCCACGCTTCATCACTTGCCTGCGGTGGTGTGTTGGTGAAGGAT 1599

QY 441 AlaArgArgLeuArgArgProArgPheAsnProTyrArgAlaPheThr1ysAlaAsn 460
 Db 1600 GCCCGAGGCTACGTGTCTCACACGCTTCAACCCATACCTGTCATTTACCAAGGCGAAT 1659
 QY 461 GluPheSerPheGlnGlnGln1aGlnGln1aGlnGln1aArgArgGln1aArg1ysArgPro1ys 480
 Db 1660 GAGTCTCTCTTCCAGAGAGAGAGCTGAGCAAAATCAGCGCGGAGAGAAACGTCACAAAG 1719
 QY 481 ThrAsnGln1aPheGlyAsn1ysArg 489
 Db 1720 ACTAATCAGAGATTCGTAATAAAG 1746
 RESULT 8
 US-09-951-535-3
 ? Sequence 3, Application US/09951535
 ? Publication No. US20030049802A1
 ? GENERAL INFORMATION:
 ? APPLICANT: ZIEGLER, PETRA
 ? APPLICANT: EGGELENG, LOTHAR
 ? APPLICANT: SAHM, HERMANN
 ? APPLICANT: THIERBACH, GEORG
 ? TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
 ? TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
 ? FILE REFERENCE: 21123/282415/MAS
 ? CURRENT APPLICATION NUMBER: US/09/951,535
 ? PRIOR FILING DATE: 2001-09-14
 ? PRIOR APPLICATION NUMBER: 09/431,099
 ? PRIOR FILING DATE: 1999-11-01
 ? PRIOR APPLICATION NUMBER: DE 199 41 478.5
 ? PRIOR FILING DATE: 1999-09-01
 ? NUMBER OF SEQ ID NOS: 10
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ ID NO 3
 ? LENGTH: 1909
 ? TYPE: DNA
 ? ORGANISM: Corynebacterium glutamicum
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: (280)..(1746)
 ? OTHER INFORMATION: thr3-Gen
 US-09-951-535-3
 Alignment Scores:
 Pred. No.: 1,71e-263 Length: 1909
 Score: 2432.00 Matches: 489
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 DB: 10
 US-09-963-521-2 (1-489) x US-09-951-535-3 (1-1909)
 QY 1 MetLeuSerPhe1a1aThr1eupArgGly1aArg11eSerThrVal1aAspAla1a1a1a 20
 Db 280 ATGTTGAATTTGGCAACCTTCGTGCGCATTTCAACAGTTGACGTCGCAAAACCGCA 339
 QY 21 ProProProSerProLeu1a1aPro11eAspLeuThrAspHisSerSerGlnVal1a1aGlyVal 40
 Db 340 CCTCGCATGCGCACATGAGCCCGCATTTATCTCACTGACATAGCAAGTGGCGGTGTG 399
 QY 41 MetLeuLeu1a1a1aArg11eGlyAsp11eLeuLeuSerSerGly1ThrSerAsnSerAsp 60
 Db 400 ATGATTTTGGCGGAGGAAATGGCATATTGCTTTCTTCAAGTACGTCANAATAGTAC 459
 QY 61 Thr1ysVal1GlnVal1aArgAlaVal1aThrSer1a1aTyrGly1eU1TyrThrHisValAsp 80
 Db 460 ACCAAGTAACAAGTTCGACGAGTACCTCTGCGTACGGTTTGTACTACACGACGTGAT 519
 QY 81 11ethrLeuAsnThr11ethr11ephethrAsn11eglyVal1GluArg1ysMetProVal 100
 Db 520 ATCACTTGAATACGATACACATCTTACCAACATCGGTGTGAGAGAAATGCGGCTC 579

QY	101	AsnValPheHisIaValaGlyIysLeuAspThrAsnPheSerIysLeuSerGluValAsp	120
Db	580	AAAGTGTTATATTGGAGCAAGTTGGACACCAACTCTCCAACTGCTGAGGTTGAC	639
QY	121	ArgLeuIleArgSerIleGlnIaGlyValaThrProGlnValaGluIysIleLeu	140
Db	640	CGTTGATCCGTTCCATTACAGCTGGTGGACCCGCCCTGAGGTTGCCAGAAATCTTG	699
QY	141	AspGlnLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyThrAla	160
Db	700	GAGAGATTGGAGCAATCCCTCGCTTTAGTTTCCCTGTTGCGTTGCTGGCTGGCA	759
QY	161	MetMetGlyGlyValaValaAlaValaLeuLeuGlyGlyGlyTyrGlnValSerIleIleAla	180
Db	760	ATGATGAGTGAGTCTGTGTGTGGCTTGGTGGTGGATGGATGGCAAGGTTTCCCTAATGTCT	819
QY	181	PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIysIysGlyLeuPro	200
Db	820	TTTATATACCGCGTTACGATCATGTGCCAGAGCTCATTTTGGGAAAGAGGTTTGCT	879
QY	201	ThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr	220
Db	880	ACTTCTTCCAAAGTTGTGGTGTATTATTTGACACGCTCCGACATCGATTCTTAT	939
QY	221	SerLeuAlaLeuGlnPheGlyLeuGlnIleIysProSerGlnIleAlaSerGlyIle	240
Db	940	TCTTTGGCGTTGCAMTTTGCTTGATGATCAACGAGCGAGATCATGCACTTGAAAT	999
QY	241	ValIValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla	260
Db	1000	GTTTGCTGTTGGCAGAGTTTGACACTCGGCAATCTTCGAGAGCGGATCATCGGGCCT	1059
QY	261	ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyGlyIleValAla	280
Db	1060	CCGGGACGACGACAGTCCAGATTTTTCGAAACACTCTGTTTACCGGCGGCAATTGTCT	1119
QY	281	GlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuHisValMetLeuProAlaMetGlu	300
Db	1120	GGCGGGGTTTGGGCAATTCAGCTTCTGAAATCTTGCAATGATGTCCTGCGCATGGAG	1179
QY	301	SerAlaAlaAlaProAsnThrSerSerThrPheAlaArgIleIleAlaGlyValaThr	320
Db	1180	TCCGCTGCAGCACTTAATTAATTCGTCAATTCGCCCATTAATCGCGGGGCTCAAC	1239
QY	321	AlaAlaAlaPheAlaValGlyCysTyrAlaGlnTyrSerSerValIleIleAlaGlyLeu	340
Db	1240	GCAGCGGCTTCGCGAGTGGTGTAAAGCGGAGTGTCTCTGGATTAATTGGCGGCTT	1299
QY	341	ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValValIyrLeuGlyProValSer	360
Db	1300	ACTGGCGTGAAGGTTCTGGCGTTTAACTCTTCGTTGTTTAAAGCCCGCTCTCT	1359
QY	361	AlaAlaAlaIleAlaAlaThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgArgPhe	380
Db	1360	GCCGCTGCAGATTGCGTGAACAGCAGATTGGTTCACTGGATGTTTCTGCCCGTCGATTC	1419
QY	381	LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla	400
Db	1420	TTGATTTCCACCGTTGATGTTGGCGATTGCCGCAATCACCAATAGCTTCAGGCTGACA	1479
QY	401	IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle	420
Db	1480	ATTTAACCGGGAATGTACGCCACCTGATATATCAAAACATCTCAAGGATTCAACCAACTT	1539
QY	421	AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGluTyrIle	440
Db	1540	GCGGTGCTTTAGCGACAGCTTCATCACTTCCGCTGGCGGAGTTTGGGTGATGTGATT	1599
QY	441	AlaArgArgLeuArgArgProProArgPheAsnProTyrArgAlaPheThrIysAlaAsn	460
Db	1600	GCCCGAGCGTACGTGCTTACACAGCGCTTCAACCAATACGTTGATTTACCAAGGCAAT	1659

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QY      461 GluPheSerPheGlnGlnAlaGlnGlnAsnGlnArgGlnArgGlnArgLysArgProLys 480
Db      1660 GAGTTCCTCCCTTCAGAGAGAGAGCTGACGAATTCAGCGCGGACAGAGAAAGCTCCAAAG 1719

QY      481 ThrAsnGlnArgPheGlyAsnLysArg 489
Db      1720 ACTAATCAGAGATTCGGTAAATTAAGG 1746

RESULT 9
US-10-224-574-11
/ Sequence 11, Application US/10224574
/ Publication No. US20040101837A1
/ GENERAL INFORMATION:
/ APPLICANT: Forschungszentrum Jilich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
/ APPLICANT: P. Peters-Wendisch
/ TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the
/ TITLE OF INVENTION: L-Serin, improved process for the microbial manufacture of L
/ FILE REFERENCE: PZJ-9912-PCT
/ CURRENT APPLICATION NUMBER: US/10/224,574
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 1909
/ TYPE: DNA
/ ORGANISM: C. glutamicum ATCC 13 032
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (280)..(1746)
/ OTHER INFORMATION: thr E (Threonin-exportcarrier)
US-10-224-574-11

Alignment Scores:
Pred. No.: 1 71e-263 Length: 1909
Score: 2432.00 Matches: 489
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-963-521-2 (1-489) x US-10-224-574-11 (1-1909)

QY      1 MetLeuSerPheAlaThrLeuArgGlyArgLysSerThrValAspAlaAlaLysAlaAla 20
Db      280 ATGTTGAGTTTGGGAGCCCTTCGTCGGCGCATTTCAACAGTTGAGCGTCAAAAGCCGCA 339

QY      21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
Db      340 CTCGCCGATCGCCACATGAGCCCGATGATCTCACTACCAATGATCAAGTGGCCGGTGTG 399

QY      41 MetAsnLeuAlaAlaArgLysAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
Db      400 ATGAATTGGCTGGGAGAAATTTGGGCAATTTTGGTTCTTCAGGTACGTCAAAATAGTGAC 459

QY      61 ThrLysValGlnValAlaArgAlaValThrSerAlaTyrGlyLeuTyrThrHisValAsp 80
Db      460 ACCAAGGTACAAAGTTCAGACGAGTCACTCTCGGACGGTTGTACTACAGCGACGTGGAT 519

QY      81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgLysMetProVal 100
Db      520 ATACGTTGATAGAGACACCATCTTCAACCAATCGTGTGGAGAGAGAGATGCCGCTC 579

QY      101 AsnValPheHisValAlaGlyLysLeuAspThrAsnPheSerLysLeuSerGluValAsp 120
Db      580 AACGCTTTCATATGTTGAGCAAGTTGGACACCAACTTCTCCAAACTGCTGAGGTGAC 639

QY      121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProGluValAlaGluLysIleLeu 140
Db      640 CGTTTATCGTTCCATTCAGGCTGGTGGACCCCGCTGAGGTGCCGAGAAATCTTG 699

QY      141 AspGluLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrPala 160

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Db 700 GACGAGTTGAGCAATCCCTGGCTCTTANGTTTCCCTGCTTGGCTTGGCTGGGCA 759
Qy 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyGlyTyrGlnValSerLeuIleAla 180
Db 760 ATGATGGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819
Qy 181 PheIleThrAlaIleThrIleIleAlaThrThrSerPheLeuGlyLysLysGlyLeuPro 200
Db 820 TTTATTAACCGCGTTGACGATCATGTCACGACGATTTTGGGAAAGAGGCTTCCCT 879
Qy 201 ThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProIleSerIleAlaTyr 220
Db 880 ACTTCTTCCAAATGTTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 939
Qy 221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLysProSerGlnIleIleAlaSerGlyIle 240
Db 940 TCTTGGCGTTGCAATTTGCTTGAATCAACCGACGACGACGACGACGACGACGACGACGAC 999
Qy 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260
Db 1000 GTTGTGCTGTTGGCAGGTTTGACCTGTCATCTTGACGAGCAGGACGACGACGACGACGAC 1059
Qy 261 ProValThrAlaSerAlaArgPheGlnThrLeuLeuPheThrGlyGlyIleValAla 280
Db 1060 CCGGTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1119
Qy 281 GlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuHisValMetLeuProAlaMetGly 300
Db 1120 GGCGTGGGTTTGGGCAATTCAGCTTTCGAAATCTTGCAATGTCATGTCATGTCATGTCATG 1179
Qy 301 SerAlaAlaAlaProAlaThrSerSerSerThrPheAlaArgIleIleAlaGlyValThr 320
Db 1180 TCCGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1239
Qy 321 AlaAlaAlaPheAlaValGlyCysTyrAlaGlnTyrSerSerValIleIleAlaGlyLeu 340
Db 1240 GCAAGCGCTTCGACGATGCTGTTTACGCGAGTGTCTCGTGATATTTGGCGGCTT 1299
Qy 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProValSer 360
Db 1300 ACTGGGTGATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1359
Qy 361 AlaAlaAlaIleAlaAlaThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgPhe 380
Db 1360 GCGGTGCGATGTCGACACGACGATGCTTTCACGATGCTGCTGCTGCTGCTGCTGCTGCT 1419
Qy 381 LeuIleProPheLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
Db 1420 TTGATTCACGCTGATGTTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1479
Qy 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
Db 1480 ATTATCCCGGAAATGACGACGACGCTGAAATGATCAACATCATGCTTCCCAACATT 1539
Qy 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGlnTyrIle 440
Db 1540 GGGGTGCTTTCACGATCTTCATCATCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 1599
Qy 441 AlaArgArgLeuArgArgProProArgPheAsnProTyrArgAlaPheThrLysAlaAsn 460
Db 1600 GCGCGACGCTACGTCGTCACACGCTTCAACCCATACCGTGATTTTACCAAGCGAT 1659
Qy 461 GluPheSerPheGlnGlnAlaGlnIleAsnGlnArgArgGlyArgLysArgProLys 480
Db 1660 GAGTCTCTCTCCAGAGAACTGACGAAATCAAGCGCGGACAGAAACGCTCCAAAG 1719
Qy 481 ThrAsnGlnArgPheGlyAsnLysArg 489
Db 1720 ACTAATCAGAGATTCGTAATAAAG 1746

RESULT 10
US-09-951-536-1
; Sequence 1, Application US/09951536

Patent No. US20020107378A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, IOTHAIR
; APPLICANT: SAHM, HERMAN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THR GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; TITLE OF INVENTION: USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282414/MAS
; CURRENT APPLICATION NUMBER: US/09/951,536
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thr-Gen
; US-09-951-536-1

Alignment Scores:

Pred. No.:	3,136-263	Length:	2817
Score:	2432.00	Matches:	489
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-963-521-2 (1-489) x US-09-951-536-1 (1-2817)

Qy 1 MetLeuSerPheAlaThrLeuArgGlyArgIleSerThrValAspAlaAlaValAla 20
Db 398 ATGTTGAGTTTGGACGCTTCGTTGCGCGCATTTCCACAGTTGACGCTGCAAAAGCCGCA 457
Qy 21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
Db 458 CCTCGGCATGCGCACTGACCCCGATGATCTCACTGACCATAGTCAAGTGGCGGTGCTG 517
Qy 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
Db 518 ATGATTTGGCTGCGAGAAATGGGCAATTTGCTTCTTCAGGTACGTCAACAGTAT 577
Qy 61 ThrLysValGlnValArgAlaValThrSerAlaTyrGlyLeuTyrTyrThrHisValAsp 80
Db 578 ACCAAGGTGCAAGTTGCGAGCGGTGACCTCTGCTGATGGCTGTACTATACGATGTGAT 637
Qy 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgLysMetProVal 100
Db 638 ATCAGTGAATACATACATACATCTTCACCAACATCGGTGAGAGAGAGATGCGGTG 697
Qy 101 AsnValPheHisValValGlyLysLeuAspThrAsnPheSerLysLeuSerGlnValAsp 120
Db 698 AACGTTTCAATGTTGCGGCAAGTTGACACCAACTTCTCCAAACTGTCTGAGGTTGAC 757
Qy 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGlnValAlaGlnLysIleLeu 140
Db 758 CGTTTGAATCCGTTTCAATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 817
Qy 141 AspGlnLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrPal 160
Db 818 GACGAGTTGAGACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
Qy 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyGlyTyrGlnValSerLeuIleAla 180
Db 878 ATGATGGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 937
Qy 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysLysGlyLeuPro 200

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Db      938 TTTTATACCGGCTTCACATCATTCGCCACGACGTCATTTTGGGAAACAAAGGTTGCT
Qy      201 ThrPhepGlnAsnValAlaGlyGlyPheIleAlaThrLeuProAlaSerIleAlaIle
Db      998 ACTTCTTCCAAATGTTGTTGGTTTATTTGTCACGCTGCTGATTCATTCCTTAT
Qy      221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLysProSerGlnIleIleAlaSerGlyIle
Db      1058 TCTTGGCGGTGCAATTTGCTTGAATCAACCCGACCATCATCGCATTCGGAATT
Qy      241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAsnGlyIleThrGlyAla
Db      1118 GTTGTCCTGTTGGCAGGTTTACACTTGTGCAATCTTCGACGACGCGCATACGCGGCT
Qy      261 ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIleValAla
Db      1178 CCGGTGACGACGACGACGATTTTGGAAACACTCCCTGTTTACCGGCGGATGTTGCT
Qy      281 GlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuHisValMetLeuProAlaMetGln
Db      1238 GGGCTGGGTTTGGCATTCAGCTTTCGAATCTTGATGATGATGCTGCGCATGAG
Qy      301 SerAlaAlaAlaProAsnIleSerSerThrPheAlaArgIleIleAlaGlyValThr
Db      1298 TCCGCTCGACGACCTAATTTATTCCTACATTCGCCCGCATTCGCTGGTGGCGTACC
Qy      321 AlaAlaAlaPheAlaValAlaGlyCysTyrAlaGlnTrpSerSerValIleIleAlaGlyLeu
Db      1358 GCAGCGGCTTCGACGAGGTTGTTACGCGGAGTGGCTCGGATTAATTCGGGGCTT
Qy      341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValAlaTyrLeuGlyProValSer
Db      1418 ACAGCGGTGATGGGTTCTGGGTTTATTACCTCTCTGTTTATTAGGCCCGCTCTCT
Qy      361 AlaAlaAlaIleAlaIleAlaThrAlaValAlaGlyPheThrGlyGlyLeuLeuAlaArgPhe
Db      1478 GCGCGTGGCATTTGCTGCAACAGAGTTGGTTTCACTGGTGGTGGTGGCTGGCGATTC
Qy      381 LeuIleProLeuLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla
Db      1538 TTGATTCACCGTTGATTTGGCGATGGCGGATGCACCAATGCTTCCAGGCTACGCA
Qy      401 IleTyrAlaGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle
Db      1598 ATTTCACCGGGAATGAGCGCACCTTGAATGATCAACACTCATGGGTTTCCACCAACTT
Qy      421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValLeuGlyGlnTrpIle
Db      1658 GCGGTTGCTTTAGCCACTGCTTATCATCTTCCGCTGGCGTGGTTTGGTGGAGTATT
Qy      441 AlaArgArgLeuArgArgProProArgPheAsnProTyrArgAlaPheThrIleAlaAsn
Db      1718 GCCCGACGAGTACGTGCTCCACACGCTTCAACCCATACGTCATTTTACCAAGGAGAT
Qy      461 GlnPheSerPheGlnGlnGlnAlaGlnGlnAsnGlnArgGlnArgGlnArgProLys
Db      1778 GAGTTCTCTCCAGGAGGAGCTGAGCAGAAATCAGCGCGGCAAGAAAAGCTCCAAAG
Qy      481 ThrAsnGlnArgPheGlyAsnLysArg 489
Db      1838 ACTTATCAAAAGATTCGTAAATATAAAG 1864

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; TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282413/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: three-Gen
; US-09-963-521-1

Alignment Scores:
Pred. No.: 3,13e-263 Length: 2817
Score: 2432.00 Matches: 489
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-963-521-2 (1-489) x US-09-963-521-1 (1-2817)

Qy      1 MetLeuSerPheAlaThrLeuArgGlyArgIleSerThrValAspAlaIleAlaAla
Db      398 ATGTTGATTTTTCGACCCCTTCGTCGTCGATTCACACATTCGTCGCAAAACCGCA
Qy      21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal
Db      458 CCTCCCGCATCGGACACTAGCCCGCATGATCTCACTGACCATAGTCAAGTGGCGGTGTG
Qy      41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerGlyThrSerAsnSerAsp
Db      518 ATGAAATTTGCTCGAGAAATGGCGAATTTGCTTCTTCAAGTACGTAACACATGAT
Qy      61 ThrLysValGlnAlaAlaArgAlaValThrSerAlaTyrGlyLeuTyrThrHisValAsp
Db      578 ACCAAGTGAAGTGAAGGAGTGACCTCGCTATGCGCTGATACATACGATGATGAT
Qy      81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgLysMetProVal
Db      638 ATCAGCTGAAATACGATACACATCTTCAACCAACATGAGTGTGAGAGAAATGCCGCTC
Qy      101 AsnValPheHisValValAlaGlyLysLeuAspThrAsnPheSerLysLeuSerGlyValAsp
Db      698 AACGTTTTCATGTTTGTGGCAGAGTTGACACCAACTTCTCCAAACTGCTGAGGTTGAC
Qy      121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGlnValAlaGlnLysIleLeu
Db      758 CGTTTATCCGTTCCATTCACGCTGAGTGTCTACCCCGCTGAGGTTCCCGAGAAATTTCTG
Qy      141 AspGlnLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrPala
Db      818 GACGAGTTGAGCAACATCGCTGCTTATGTTTCCGTTGCGTGTGCTGGCGGCA 877
Qy      161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyTyrGlnValSerLeuIleAla
Db      878 ATGATGGGTGGCGGCTTCTGCTGCTGTGGGTGGATGCGAGGTTTCCCTAATTTGCT
Qy      181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysLysGlyLeuPro
Db      938 TTTATTTACCGCGTTCACGATTCATTCGACGACGATCTTTTGGAAAGAGGTTTGCTT
Qy      201 ThrPhepGlnAsnValAlaGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr
Db      998 ACTTCTTCCAAATGTTGTTGGTTTATTTGTCACGCTGCTGATTCATTCCTTAT

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OY 221 SerLeuAlaLeuGlnPheGlyLeuGluLeuProSerGlnIleIleAlaSerGlyIle 240
Db 1058 TCTTTGGCGCTTGGAAATTGGTCTTGAGATCAAAACCGAGCATCATCGCATTCGGAAAT 1117
OY 241 ValValIleuLeuAlaGlyLeuThrIleValIleGlnSerIleuGlnAspGlyIleThrGlyAla 260
Db 1118 GTTGTGCTGTTGGAGGTTTGACACTTGTCMACTCTGACAGAGCGGCACTACAGGCGCT 1177
OY 261 ProValIleuLeuAlaSerAlaArgPheGlyThrIleuLeuPheThrGlyIleValAla 280
Db 1178 CCGGTGACAGCAATGACCATTTTGGAAACATCTCTGTTACCGCGGATTTGCT 1237
OY 281 GlyValIleuLeuGlyIleGlnIleuSerGlnIleuIleuIleuIleuIleuIleuIleu 300
Db 1238 GGCGTGGGTTTGGCATTCAGCTTCTGAAATCTTGACATGTCATGTTGCCGTCATGAG 1297
OY 301 SerAlaAlaIleuProAsnIleuSerSerThrPheAlaArgIleIleAlaGlyIleValThr 320
Db 1298 TCCGCTGACAGCACTAATTTGCTGTCACATTCGCGCATTCGCTGAGGCGTACC 1357
OY 321 AlaAlaAlaPheAlaValIleGlyCysTyrAlaGluIleuPheSerValIleIleAlaGlyLeu 340
Db 1358 GCAGCGGCTTGGAGTGGTGTTCACCGGAGTGTCTCGGATTAATTCGCGGCTT 1417
OY 341 ThrAlaIleuLeuGlySerAlaPheTyrTyrIleuPheValIleTyrLeuGlyProValSer 360
Db 1418 ACTGCGCTGATGGGTTCTGCGTTTATTAACCTTCCTGTTTATTAAGGCCGCTCTCT 1477
OY 361 AlaAlaAlaIleAlaIleThrAlaValIleGlyPheThrGlyIleuLeuAlaArgPhe 380
Db 1478 GCCGCTGGATGTGTGCAACAGCAGTGGTTCACGAGGTTGCTTGGCCGTCGATTC 1537
OY 381 LeuIleProPheIleuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
Db 1538 TTGATTCACCGCTTATGTTGGCGATTCGCGGACATCAACCAATGCTTCCAGGTCATACA 1597
OY 401 IleTyrArgGlyMetTyrAlaIleThrIleuAsnAspGlnIleuMetGlyPheThrAsnIle 420
Db 1598 ATTAAACCGAGATGTACGCCACCTTGAAATGATCAACCACTCATGGTTTCAACCAACTT 1657
OY 421 AlaValAlaIleuAlaIleThrAlaSerSerIleuAlaAlaGlyValIleuGlyIleuIle 440
Db 1658 GCGGTGCTTTAGCCACGCTTCATCATCTGCGCTGGCGTGGTGGTGGTGGTGGTGGTGGT 1717
OY 441 AlaArgArgLeuArgArgProArgPheAsnProTyrArgAlaPheThrIleuIleAsn 460
Db 1718 GCCGCAAGCTACGTCGTCACCAACGCTTCAACCCATACCGTGCATTTACCAAGCGCAAT 1777
OY 461 GluPheSerPheGlnGluGluAlaGluGlnAsnGlnArgGlnArgGlyArgProIle 480
Db 1778 GAGTCTGCTCTCCAGAGAGAGAGCTGACGAGATTCAGCGCGGAGAGAGAGAGAGAGAGAG 1837
OY 481 ThrAsnGlnArgPheGlyAsnIleuArg 489
Db 1838 ACTAATCAAGATTCGATTAATAAAG 1864

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; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC14752
; NAME/KEY: CDS
; LOCATION: (398) ..(1864)
; OTHER INFORMATION: thrS gene
; US-09-834-721-1
Alignment Scores:
Pred. No.: 3,13e-263 Length: 2817
Score: 2432.00 Matches: 489
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-963-521-2 (1-489) x US-09-834-721-1 (1-2817)
OY 1 MetLeuSerPheAlaThrIleuArgGlyArgIleSerThrValAspAlaValAla 20
Db 398 ATGTTGAGTTTGGAGCCCTTGTGCGCATTCACAGTTGACGCTGCAAAAGCCGCA 457
OY 21 ProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
Db 458 CTTCCGCCATCGCCACTAGCCCGCATTCATCTACATGACATGCAAGTGGCGGTGTG 517
OY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
Db 518 ATGAATTTGGCTGGAGATATGGAGATTTGGCTTTCTTCAGGTACGTCMAAGATGAT 577
OY 61 ThrIleValGlnValAlaArgAlaValThrSerAlaTyrGlyLeuTyrTyrThrHisValAsp 80
Db 578 ACCAAGGTGCAAGTTCAGCGGTGACCTTCGATGAGCTGTTACTATACCATGTGAT 637
OY 81 IleThrIleuAsnThrIleThrIlePheThrAsnIleGlyValIleuArgIleMetProVal 100
Db 638 ATCAGTTGATATGATCATCATCATCTTCCAACTCGGTGAGAGAGATGCGGCTC 697
OY 101 AsnValPheHisValValGlyIleuLeuAspThrAsnPheSerIleuSerGlyValAsp 120
Db 698 AACGTTGATCGTTCATTCAGGTGGCAAGTTGGACACCACTTCTCCAACTGTGAGGTTGAC 757
OY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProGluValAlaGluIleuIleu 140
Db 758 CGTTTGATCCGTTCCATTCAGGCTGTGTCTACCCGCTGAGCTTGGCCAGAAATTTCTG 817
OY 141 AspGluLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaIleuLeuGlyTyrAla 160
Db 818 CACGAGTTGGAGCAATCCGCTCCGCTTATGTTTCCGTTGCGTGGTGGTGGTGGTGGTGGT 877
OY 161 MetMetGlyIleValAlaValAlaValLeuLeuGlyIleGlyIleGlnValSerIleuIleAla 180
Db 878 ATGATGAGTGGGCGCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 937
OY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIleuIleuIleuIleuPro 200
Db 938 TTATATTCGCGCTTACATCATCTTCCACGACGTCAATTTTGGAAAGAGGTTTGCTT 997
OY 201 ThrPhePheGlnAsnValAlaGlyIlePheIleAlaThrLeuProAlaSerIleAlaTyr 220
Db 998 ACTTCTTCCAAAAGTTGTTGGTGGTTTATTTGACAGCTGCTGCAATCGATTTGCTTAT 1057
OY 221 SerLeuAlaLeuGlnPheGlyLeuGluIleuProSerGlnIleIleAlaSerGlyIle 240
Db 1058 TCTTTGGCGCTTGGAAATTGGTCTTGAGATCAAAACCGAGCATCATCGCATTCGGAAAT 1117
OY 241 ValValIleuLeuAlaGlyLeuThrIleValIleGlnSerIleuGlnAspGlyIleThrGlyAla 260
Db 1118 GTTGTGCTGTTGGAGGTTTGACACTTGTCMACTCTGACAGAGCGGCACTACAGGCGCT 1177

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Alignment Scores:			
Pred. No.:	3.13e-263	Length:	2817
Score:	2432.00	Matches:	489
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
Db:	9	Gaps:	0
US-09-963-521-2 (1-489) x US-09-783-388-1 (1-2817)			
QY	1 MetLeuSerPheAlaThrLeuArgGlyValArgIleSerThrValAspAlaAlaValAspAla	201	
Db	398 ATGTTGAGTTTGGGACCCCTTCGGGGCGCATTTCAACAGTTACACCTGGCAAAAGCGCA	439	
QY	21 ProProPseProLeuAlaProIleAspLeuThrAspIleSerGlnValAlaGlyVal	404	
Db	458 CCTCGCGCATGGCCACTAGCCCGCATTTGATCTCACTGACCATATGTCAGTGGCCGGTGTG	513	
QY	41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp	607	
Db	518 ATGAAATTTGGGTGGAGAAATTTGGCATATTTTCTTTCTTCAAGTACGTCAAAACATGAT	574	
QY	61 ThrIleValGlnValArgAlaValThrSerAlaTyrGlyLeuTyrTyrThrIleValAsp	800	
Db	578 ACCAAGGTGCAAGTTGACGGGTGACCTCGCGTATGGCTGTACATACATGCAATGTGAT	633	
QY	81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGlnArgIleMetProVal	1010	
Db	638 ATCAGCTTGAATTCAGATCACCATTCTTCAACATATGGTGTGAGAGGAAATTCGGCTC	699	
QY	101 AsnValPheIleValValGlyIleLeuAspThrAsnPheSerIleLeuSerGlnValAsp	1212	
Db	698 AACGTGTTTATGTTGTGGGCAAGTTGGACACCACTTCTCCAACTGTCTGAGGTTGAC	751	
QY	121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGlnValAlaGlnIleLeu	1414	
Db	758 CGTTTATCCGTTCCATTCAGGTGTGTGTACCCCGCTGAGGTTGCCGAGAAATTCGTG	811	
QY	141 AspGlnLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyIlePheAla	1616	
Db	818 GACGAGTTGAGCAATTCGCTGCTTTATGTTTCCCTGTTCGCTGTGGCGTGGCGCA	877	
QY	161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyIleTyrGlnValSerLeuIleAla	1818	
Db	878 ATGATGGGTGGCGCTGCTGTGCTGTGGTGGTGGATGGCAGTTTCCCTAATTCCT	939	
QY	181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIleValGlyLeuPro	2020	
Db	938 TTATATTAACCGCGTTTCCAGATTCATTCGACGATGATTTTGGGAAAGAGGTTTGCTT	999	
QY	201 ThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaIleTyr	2222	
Db	998 ACTTCTTCCAAATATTTGTGTGTGTATTTATGGCAGCGCTGTGATTCATATTCATAT	1059	
QY	221 SerLeuAlaLeuGlnPheGlyLeuGlnIleTyrProSerGlnIleIleAlaSerGlyIle	2424	
Db	1058 TCTTTGGCGTTGCAATTTGTCTTGTAGATCAAAACCGACCGCATATGCAATTCGAAAT	1111	
QY	241 ValValLeuLeuAlaGlyLeuThrIleValGlnSerLeuGlnAspGlyIleThrGlyAla	2626	
Db	1118 GTTGTGCTTGTGGCAGGTTTGAACCTTGTGCATCTTCGACGACGCGCATACAGGCGCT	1179	
QY	261 ProValThrAlaSerAlaThrPhePheGlnThrIleLeuPheThrGlyIleValAla	2828	
Db	1178 CCGGTACACGACGACGACGATTTTGTAAACATCTCGTTTACCGGGCGCATTTGCTT	1239	
QY	281 GlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuIleValMetLeuProAlaMetGln	3030	
Db	1238 GGGGTGGGTTTGGGCGATTCAGCTTCTGAATCTTGATGATCATGCTTGGCTGGCATGGAG	1299	
QY	301 SerAlaAlaAlaProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyGlyValThr	3201	

Db 1298 TCCGCTGCAGACCTAATTAATTCGTCTACATTCGCCGCAATTAATTCGCTGTCGCTCACC 1357
 QY 321 AAlaAlaAlaPheAlaValAlaGlyCysTyrAlaGluTyrSerSerValIleIleAlaGlyLeu 340
 Db 1358 GCAAGCGGCTTCCAGTGGTTCGTACGCGAGTGGTCCCTCGGTATTAATTCGGGGCTT 1417
 QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValValTyrLeuGlyProValSer 360
 Db 1418 ACTGCGCTGATGGTCTCGGTTCATTAATTCCTTCGTTTATTAATTAATTAATTAATTAATTA 1477
 QY 361 AAlaAlaAlaIleAlaAlaThrAlaValAlaGlyPheThrGlyGlyLeuLeuAlaArgPhe 380
 Db 1478 GCGGCTGCGATGTGTGACAGAGGTTGGTTTACATGAGTTCGTTGCTTGCCTGCAATTC 1537
 QY 381 IleuIleProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
 Db 1538 TTGATTCACCGTTGATGTGGGATTCGCCGATCACACCAATGCTTCACAGGCTCAACA 1597
 QY 401 IleTyrArgIleMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
 Db 1598 ATTACCGCGAATGTAGCGCACTTGAATGATCAACACATCATGGGTTTCACCAACATTT 1657
 QY 421 AlaValAlaLeuAlaThrAlaSerSerLeuAlaAlaGlyValValIleuGlyGluTyrIle 440
 Db 1658 GCGGTTCTTTAGCCACGCTTCACTACCTGCGCTGCGTTCGTTGGTGAATGATTT 1717
 QY 441 AlaArgIleuArgArgProProArgPheAsnProTyrArgAlaPheThrIleAsn 460
 Db 1718 GCCCGAGGCTACGCTCCACCAACGCTTCAACCATACGTCGATTAACCAAGCGCAAT 1777
 QY 461 GluPheSerPheGlnGluGluAlaGluGlnAsnGlnArgGlnArgGlyArgProLys 480
 Db 1778 GAGTTCCTCTCCAGCGAGGAGCTGAGCAATCAAGCGCGCAGAGAAAGTCCAAAG 1837
 QY 481 ThrAsnGlnArgPheGlyAsnLysArg 489
 Db 1838 ACTAATCAAGATTCGGTAATTAAGG 1864

RESULT 14

US-09-951-535-1

; Sequence 1, Application US/09951535
 ; Publication No. US20030049802A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZIEGLER, PETRA
 ; APPLICANT: SAHM, HERMANN
 ; APPLICANT: EGGELING, LOTMAR
 ; APPLICANT: THIERSCH, GREGG
 ; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
 ; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
 ; FILE REFERENCE: 21123/282415/MAS
 ; CURRENT APPLICATION NUMBER: US/09/951,535
 ; CURRENT FILING DATE: 2001-09-14
 ; PRIOR APPLICATION NUMBER: 09/431,099
 ; PRIOR FILING DATE: 1998-11-01
 ; PRIOR APPLICATION NUMBER: DE 199 41 478.5
 ; PRIOR FILING DATE: 1999-09-01
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2817
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (398)..(1864)
 ; OTHER INFORMATION: thrB-Gen
 ; US-09-951-535-1

Alignment Scores:

Pred. No.: 3, 13e-263 Length: 2817
 Score: 2432.00 Matches: 489
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-963-521-2 (1-489) x US-09-951-535-1 (1-2817)

QY 1 MetLeuSerPheAlaThrLeuArgIleArgIleSerThrValAspAlaValAla 20
 Db 398 ATCTTAAGTTTCCGACCCCTGTCGCGCATTTCAACAGTTCAGCTGCAAGCGCGCA 457
 QY 21 ProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40
 Db 458 CTTCCCGCATCGCCACATGAGCCCGATTCATCACTACATATGTCAGAGTGGCGGTGG 517
 QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
 Db 518 ATGAATTTGGCTCGAGAAATGGGATATTTTCTTCTTCAGGTACGTCAACAGTGCAT 577
 QY 61 ThrIleValGlnValArgAlaValThrSerAlaTyrGlyLeuTyrTyrHisValAsp 80
 Db 578 ACCAAGTGCAGATTCAGAGCGGTGACCTCGCGTATGCGCTGTACTATACGATGTGGAT 637
 QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValGluArgLysMetProVal 100
 Db 638 ATCAGCTTGAATACGATCACCATCTTCCACCAACATCGGTGAGAGAGAGATCCCGGTC 697
 QY 101 AsnValPheHisValValAlaGlyLysLeuAspThrAsnPheSerLysLeuSerGluValAsp 120
 Db 698 AACGTGTTCAATGTTGGGCGAATTTGACACCAACTTCTCAAACTGTCTGAGGTTCAC 757
 QY 121 ArgLeuIleArgSerIleGlnAlaGlyAlaThrProProGluValAlaGluLysIleLeu 140
 Db 758 CGTTGATCCGTTCCATTCAGCTGAGTGCACCCGCTGAGGTTCGCAAGAAATTCGTG 817
 QY 141 AspGluLeuGluGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrAla 160
 Db 818 GACGAGTTGGAGCAATGCGCTCTTATGTTTCCTGTTGGTTCCTTGGCTGGCGGCA 877
 QY 161 MetMetGlyGlyValAlaValAlaLeuLeuGlyGlyTyrGlnValSerLeuIleAla 180
 Db 878 ATGATGGTGGCGCTGTTGCTGTGTGTGGTGTGGATGGCAGGTTTCCCTAATTCGT 937
 QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyLysGlyLeuPro 200
 Db 938 TTATTAACCGGCTTCACATCATTCGCCACGATCATTTTGGGAAAGAGGTTTCCT 997
 QY 201 ThrPhePheGlnAsnValAlaGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr 220
 Db 998 ACTTTCCTCCAAAATGTTGTTGGTGTATTAATGCGACGCTGCGCATGATTCCTTAT 1057
 QY 221 SerLeuAlaLeuGlnPheGlyLeuGluIleLysProSerGlnIleIleAlaSerGlyIle 240
 Db 1058 TCTTTGGCGTTGCATTTGGTCTTGATCAACACGACGACGATCATGCAATCGGAATT 1117
 QY 241 ValValLeuLeuAlaGlyLeuThrLeuValGlnSerLeuGlnAspGlyIleThrGlyAla 260
 Db 1118 GTTGGCTGTTGGCAGGTTTGAACCTTGTGCAATCTGCGACAGAGCGGATCACTCCGCT 1177
 QY 261 ProValThrAlaSerAlaArgPhePheGlnThrLeuLeuPheThrGlyIleValAla 280
 Db 1178 CCGGTGACAGCAAGTGCAGATTTTGAACACTCTGTTTACCCGGCGGCAATGTGTGCT 1237
 QY 281 GlyValAlaGlyLeuGlyIleGlnLeuSerGluIleLeuHisValMetLeuProAlaMetGlu 300
 Db 1238 GCGGTGGGTTTGGGATTCAGTTCCTGAACCTTGCAATGTCATGTGCTCCCATGGAG 1297
 QY 301 SerAlaAlaAlaProAsnTyrSerThrPheAlaArgIleIleAlaGlyGlyValThr 320
 Db 1298 TCCGCTGCAGACCTAATTAATTCGTCTACATTCGCCGCAATTAATTCGCTGTCGCTCACC 1357
 QY 321 AAlaAlaAlaPheAlaValAlaGlyCysTyrAlaGluTyrSerSerValIleIleAlaGlyLeu 340
 Db 1358 GCAAGCGGCTTCCAGTGGTTCGTACGCGAGTGGTCCCTCGGTATTAATTCGGGGCTT 1417

QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValTyrLeuGlyProValSer 360
Db 1418 ACTGGCGATGGGTTCTGCGTTTATTACCTTCGTTGTTATTAGGCCCGCTCTCT 1477
QY 361 AlaAlaAlaIleAlaIleThrAlaValGlyPheThrGlyGlyLeuLeuAlaArgPhe 380
Db 1478 GCGGTGGATTGGCGAAGCAAGCAAGTGGTTCACTGGTGGTTGGTGGCCCGCGATTG 1537
QY 381 LeuIleProPheLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400
Db 1538 TTGATTCCACCGTTGATTGTTGGCCATTGCCGGCATCACCAATGCTTCCAGGTTTACA 1597
QY 401 IleTyrArgGlyMetTyrAlaThrLeuAsnAspGlnThrLeuMetGlyPheThrAsnIle 420
Db 1598 ATTAAACGGCGAATGTACGCCACCTTGATGATCAACATCAGGGTTTACCACCACTT 1657
QY 421 AlaValAlaLeuAlaIleThrAlaSerSerLeuAlaAlaGlyValAlaLeuGlyGlnTyrIle 440
Db 1658 GCGGTGGCTTTAGCCACCTGCTTCATCACTGCGCGTGGGTTGGTGGAGTGGATT 1717
QY 441 AlaArgArgLeuArgArgProProArgPheAsnProTyrArgAlaPheThrIleValAsn 460
Db 1718 GCCCGCAGGCTACGTCGTCACCAAGCTTCAACCATACCTGCTTTACCAAGCGCAT 1777
QY 461 GluPheSerPheGlnGluGlnAlaGlnGlnAsnGlnArgGlnArgGlyAsnProlys 480
Db 1778 GAGTTCTCTCTCCAGGAGGAAGTACAGATCAGCGCGCAGAGAAACGTCCAAAG 1837
QY 481 ThrAsnGlnArgPheGlyAsnIleValArg 489
Db 1838 ACTAATCAAAAGATTGCGTAATPAAAGG 1864

RESULT 15
US-10-224-574-9
; Sequence 9, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
; APPLICANT: Forschungszentrum Jlich GmbH, P. Ziegler, L. Eggeling, H. Sahm,
; APPLICANT: P. Peters-Wendisch
; TITLE OF INVENTION: Nukleotid sequences coding for proteins participating in the syt
; TITLE OF INVENTION: L-Ser, improved process for the microbial manufacture of L-ser
; TITLE OF INVENTION: genetically modified microorganism suitable for the process.
; FILE REFERENCE: F43-9912-PC1
; CURRENT APPLICATION NUMBER: US/10/224,574
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: C. glutamicum ATCC 14 752
; FEATURE:
; NAME/KEY: CDS (1867)
; LOCATION: (398)..(1867)
; OTHER INFORMATION: thr E (Threonin-exportcarrier)
US-10-224-574-9

Alignment Scores:
Pred. No.: 3,13e-263 Length: 2817
Score: 2432.00 Matches: 489
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-963-521-2 (1-489) x US-10-224-574-9 (1-2817)

QY 1 MetLeuSerPheAlaThrLeuArgGlyArgIleSerThrValAspAlaIleValAlaIle 20
Db 398 ATGTGAGTTTTCGACCCCTTCGTCGCGCATTTCAACAGTTCACGCTGCAAAAGCGCA 457
QY 21 ProProProSerProLeuAlaProIleAspLeuThrAspHisSerGlnValAlaGlyVal 40

Db 458 CCGCGCCATGCCACATAGCCCGCATGATCTCACTGACCATAGTCAAGTGGCGGTGCT 517
QY 41 MetAsnLeuAlaAlaArgIleGlyAspIleLeuLeuSerSerGlyThrSerAsnSerAsp 60
Db 518 ATGAATTTGGCTGGAGAAATGGCGAATATTTGGTTCTTCAGGATGATCAACAGATCAT 577
QY 61 ThrIleValGlnValArgAlaValThrSerAlaTyrGlyLeuTyrTyrThrHisValAsp 80
Db 578 ACCAAGGTGCAAGTTCAGCGGTACCTTCGATGAGCTGCTGACTATACCATGATGAT 637
QY 81 IleThrLeuAsnThrIleThrIlePheThrAsnIleGlyValAlaGlyLeuMetProVal 100
Db 638 ATCAGTTGAATACATACATCACCATTCTCCACCAATCGGTGAGAGCAATGCGGTCT 697
QY 101 AsnValPheHisValAlaGlyValLeuAspThrAsnPheSerIleLeuSerGlyValAsp 120
Db 698 AACGTGTTCAATGTTGGGGCAAGTTGGACCAACATTCCTCCAACTGTGAGGTTGAC 757
QY 121 ArgLeuIleArgSerIleGlnAlaGlyValaThrProProGlnValAlaGlnIleIleLeu 140
Db 758 CGTTGATCCGTTCCATTCACAGCTGCTGCTTACCCCGCTGAGGTTGCCGAGAAATTTTG 817
QY 141 AspGlnLeuGlnGlnSerProAlaSerTyrGlyPheProValAlaLeuLeuGlyTyrAla 160
Db 818 GACGAGTTGGAGCAATCGCTGCTTATGTTTCCCTGTTGCTTGGCTGGCGCA 877
QY 161 MetMetGlyGlyAlaValAlaValLeuLeuGlyGlyGlyTyrGlnValSerLeuIleAla 180
Db 878 ATGATGAGTGGCGCTGTTGCTGCTGCTGTTGGTGGTGGATGGCAGGTTTCCCTAATGCT 937
QY 181 PheIleThrAlaPheThrIleIleAlaThrThrSerPheLeuGlyIleValLeuPro 200
Db 938 TTTATTACCGGTTCAAGATCATTCGTCACACGATCTTTTGGAGAAAGAGGTTTGCT 997
QY 201 ThrPhePheGlnAsnValValGlyGlyPheIleAlaThrLeuProAlaSerIleAlaTyr 220
Db 998 ACTTCTTCCAAATGTTGTTGGTGGTTTATTATTCACACGCTGCTGCATCATGCTTAT 1057
QY 221 SerLeuAlaLeuGlnPheGlyLeuGlnIleLeuProSerGlnIleIleAlaSerGlyIle 240
Db 1058 TCTTGGCGTTGCAATTTGTTGATGATCAACCGGACCAAGATCATGCTGCGAATT 1117
QY 241 ValValLeuLeuValGlyLeuThrLeuValAlaGlnSerLeuGlnAspGlyIleThrGlyAla 260
Db 1118 GTTGTGCTGTTGGAGGTTTGCACCTTGTCATCTCTGACGACGCGCATACCGGCGCT 1177
QY 261 ProValThrAlaSerAlaArgPheGlnThrLeuLeuPheThrGlyIleValAla 280
Db 1178 CCGGTGACACCAAGTGCACGATTTTGAACAACCTCTGTTTACCGCGCGCATTTGCT 1237
QY 281 GlyValGlyLeuGlyIleGlnLeuSerGlnIleLeuHisValMetLeuProAlaMetGly 300
Db 1238 GCGGTGGTTTGGCATTCAGCTTTCGAAATCTTGATGATGATGATGATGATGATGATG 1297
QY 301 SerAlaAlaIleProAsnTyrSerSerThrPheAlaArgIleIleAlaGlyValThr 320
Db 1298 TCCGTCGACGACCATATTATTTGTCATCATTTGCCCGCATTTACGCTGGGTGCTAC 1357
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Db 1358 GCAAGCGGCTTCCAGAGGTTGTTCACCGAGTGGTCCCGGTGATTTGGCGGCTT 1417
QY 341 ThrAlaLeuMetGlySerAlaPheTyrTyrLeuPheValTyrLeuGlyProValSer 360
Db 1418 ACTGCGCTGATGGGTTCTGCGTTTATTACCTTCGTTGTTTATTAGGCCCGCTCTCT 1477
QY 361 AlaAlaAlaIleAlaIleThrAlaValAlaGlyPheThrGlyGlyLeuLeuAlaArgPhe 380
Db 1478 GCGGTGGCATTCCTGCAACAGCAAGTGGTTTCACTGGTGGTGGTGGCGCTGATTC 1537
QY 381 LeuIleProProLeuIleValAlaIleAlaGlyIleThrProMetLeuProGlyLeuAla 400


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Db      1538 TTGATTCACCGCTGATTGTGGCATTGCCGCGATCACCCCAATGCTTCAGTCTAGCA 1597
QY      401  ILeTyrArgGlyMetTyrAlaThrIleuAsnAspGlnThrIleuMetGlyPheThrAsnIle 420
Db      1598 ATTTACCGCGGATGATGACGCCACCTTGAAATGATCAAAACACTCATGGGTTTCACCAACATTT 1657
QY      421  AlaValAlaIleuAlaThrAlaSerSerIleuAlaIleValIleuGlyGluTrpIle 440
Db      1658 GCGGTTGCTTTAGCCACACTGCTTCATCACTGCCGCTGGGCTGTTTGGGTGAGTGAATTT 1717
QY      441  AlaArgArgLeuArgArgProArgPheAsnProTyrArgAlaPheThrLysAlaAsn 460
Db      1718 GCCCGCAGGCTACGTCGTCACACCGCTTCAACCATACCGTGCATTTACCAAGCGCAAT 1777
QY      461  GluPheSerPheGlnGluAlaGluGlnAsnGlnArgGlnArgLysArgProLys 480
Db      1778 GAGTTCTCTCTCCAGAGGAGAGCTGAGCAGATCAGCCGCGCAGAGAAAAAGTCCAAAG 1837
QY      481  ThrAsnGlnArgPheGlyAsnLysArg 489
Db      1838 ACTAATCAAAAGATTGGTAATPAAAAAG 1864
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Search completed: July 31, 2004, 11:47:08
Job time : 632 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 00:43:11 ; Search time 134.915 Seconds
(without alignments)
7852.389 Million cell updates/sec

Title: US-09-963-521-3

Perfect score: 1909
Sequence: 1 agcttgcatgcctgcagcgtc.....aaaccgcagccgagtcacg 1909

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 692709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
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6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1909	100.0	1909	4	US-09-431-099-3
2	1836.6	96.2	2817	4	US-09-431-099-1
3	86.6	4.5	4403765	3	US-09-103-840A-2
4	86.6	4.5	4411529	3	US-09-103-840A-1
5	47.6	2.5	7218	1	US-08-232-463-14
6	46.6	2.4	400	4	US-08-956-171E-4234
7	45.8	2.4	1230025	4	US-09-198-452A-1
8	45.6	2.4	381	4	US-08-956-171E-4023
9	44.4	2.3	237	4	US-08-956-171E-4566
10	44.4	2.3	239	4	US-08-956-171E-4543
11	44.4	2.3	239	4	US-08-956-171E-4544
12	44.4	2.3	400	4	US-08-956-171E-3531
13	44.4	2.3	400	4	US-08-956-171E-3560
14	44.4	2.3	400	4	US-08-956-171E-4198
15	44.4	2.3	411	4	US-08-956-171E-4353
16	44.4	2.3	475	4	US-08-956-171E-3621
17	44.4	2.3	6591	4	US-08-956-171E-3114
18	43.4	2.3	400	4	US-08-956-171E-3542
19	43.4	2.3	400	4	US-08-956-171E-3723
20	43.4	2.3	1171	4	US-08-956-171E-3539
21	42	2.2	339	4	US-08-956-171E-4663
22	41.2	2.2	400	4	US-08-956-171E-4029
23	40	2.1	2870	5	PCT-US93-07213-3
24	39.8	2.1	713	2	US-08-706-702-26
25	39.8	2.1	713	3	US-08-706-706-26
26	39.8	2.1	713	4	US-09-238-471-26
27	39.8	2.1	1308	4	US-09-577-424-4

28	39.8	2.1	12614	4	US-09-577-424-1	Sequence 1, Appli
29	39.2	2.1	399	4	US-09-621-976-8976	Sequence 8976, Ap
30	39.2	2.1	1232	2	US-08-189-256A-8	Sequence 8, Appli
31	39.2	2.1	1232	4	US-09-193-853-8	Sequence 8, Appli
32	39	2.0	72	2	US-08-585-585A-11	Sequence 11, Appl
33	39	2.0	81	3	US-08-685-808-10	Sequence 10, Appl
34	39	2.0	3681	1	US-08-505-860C-10	Sequence 10, Appl
35	39	2.0	4539	1	US-08-924-028A-6	Sequence 6, Appli
36	39	2.0	4539	1	US-08-119-512-1	Sequence 1, Appli
37	39	2.0	4539	1	US-08-488-015B-1	Sequence 1, Appli
38	39	2.0	4542	3	US-08-814-412-11	Sequence 11, Appl
39	39	2.0	5314	1	US-07-924-028A-4	Sequence 4, Appli
40	38.8	2.0	59	4	US-08-956-171E-4959	Sequence 4959, Ap
41	38.6	2.0	586	1	US-08-046-583-10	Sequence 10, Appl
42	38.6	2.0	586	1	US-08-184-556A-1	Sequence 1, Appli
43	38.6	2.0	586	2	US-08-331-355A-22	Sequence 22, Appl
44	38.6	2.0	586	5	PCT-US94-12364-22	Sequence 22, Appl
45	38.6	2.0	586	5	PCT-US95-07753-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-431-099-3
Sequence 3, Application US/09431099
Patent No. 6410705
GENERAL INFORMATION:
APPLICANT: Degussa-Höls AG
APPLICANT: Forschungszentrum-Joachim GmbH
TITLE OF INVENTION: New nucleotide sequences coding for the thr3 gene and process for
FILE REFERENCE: 990079 BT
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1909
TYPE: DNA
ORGANISM: Corynebacterium glutamicum ATCC13032
FEATURE:
NAME/KEY: CDS
LOCATION: (280)..(1746)
OTHER INFORMATION: thr3-Gen
US-09-431-099-3

Query Match 100.0%; Score 1909; DB 4; Length 1909;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGCTTCATGCGCGAGGTGACTTCAGAGATCCCGCTTGGACTGCTGATTTGA	60
DB	1	AGCTTCATGCGCGAGGTGACTTCAGAGATCCCGCTTGGACTGCTGATTTGA	60
QY	61	GCTGAGAGAGACTTGAATCTCAACTACGATTAAGAGTGGCGTCCATTTG	120
DB	61	GCTGAGAGAGAGACTTGAATCTCAACTACGATTAAGAGTGGCGTCCATTTG	120
QY	121	CGGCACTCCAGACCGGAGATGCTGATTCACAACTAGATTCGATTTAGGAT	180
DB	121	CGGCACTCCAGACCGGAGATGCTGATTCACAACTAGATTCGATTTAGGAT	180
QY	181	GCTGATCATCAATGGAATTCGGGCTAGATTCGATTCGATTCGATTCGATTC	240
DB	181	GCTGATCATCAATGGAATTCGGGCTAGATTCGATTCGATTCGATTCGATTC	240
QY	241	TGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC	300
DB	241	TGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC	300
QY	301	CGTGGCGGATTTCAACAGTTGACGTCGAAAGCGGACCTCGGCACTGCGC	360
DB	301	CGTGGCGGATTTCAACAGTTGACGTCGAAAGCGGACCTCGGCACTGCGC	360

Db	301	CGTGGCCGCAATTCACAGTTGACAGCTGCAGAAAAGCCGACACTCCGCAATGCGCACTAGGCC	360
QY	361	CCGATGATCTCACTGACCAATAGTCAAATGAGCGCGGTGTGATGATTTGGCTGCGAGAAATT	420
Db	361	CCGATGATCTCACTGACCAATAGTCAAAGTGGCGCGGTGTGATGATTTGGCTGCGAGAAATT	420
QY	421	GGGCATATTTTGGCTTCTTCAGAGTAAGTCAAAATATGTACACCAAGGACCAAGTTCCAGCA	480
Db	421	GGGCATATTTTGGCTTCTTCAGAGTAAGTCAAAATATGTACACCAAGGACCAAGTTCCAGCA	480
QY	481	GTGACCTCTGCGTACGGTTTGTACTACGCACGACGTGATATCACTTGAATACGATCCAC	540
Db	481	GTGACCTCTGCGTACGGTTTGTACTACACCGCACTGAGATATCACTTGAATACGATCCAC	540
QY	541	ATCTTCACCAACATCCGATGTGAGAGAGAAATATCCGCTCAACGTTTCAATGTTTAGGC	600
Db	541	ATCTTCACCAACATCCGATGTGAGAGAGAAATATCCGCTCAACGTTTCAATGTTTAGGC	600
QY	601	AAGTTGACACCAACTTCTCCAACTGTCTGAGTTGACCGTTTGAATCCGTTTCATTACG	660
Db	601	AAGTTGACACCAACTTCTCCAACTGTCTGAGTTGACCGTTTGAATCCGTTTCATTACG	660
QY	661	GCTGGTGCACCCCGCCTGAGGTTGCGGAGAAAATCTGACACGATTTGAGACAAATCCCT	720
Db	661	GCTGGTGCACCCCGCCTGAGGTTGCGGAGAAAATCTGACACGATTTGAGACAAATCCCT	720
QY	721	GCGTCTATGAGTTTCCCGTTCGCTTGACGTTGGCGCAATGATAGGTTGCTGTGTGCT	780
Db	721	GCGTCTATGAGTTTCCCGTTCGCTTGACGTTGGCGCAATGATAGGTTGCTGTGTGCT	780
QY	781	GTGCTGTTGGGTGTGATGCGAGGTTTCCCTAATGCTTTTATTAACCGGTTCAAGATC	840
Db	781	GTGCTGTTGGGTGTGATGCGAGGTTTCCCTAATGCTTTTATTAACCGGTTCAAGATC	840
QY	841	ATTGCGACAGCATTTTGTGGAAAAGAGGCTTGTGCTACTTCTTCCAAAATAGTGT	900
Db	841	ATTGCGACAGCATTTTGTGGAAAAGAGGCTTGTGCTACTTCTTCCAAAATAGTGT	900
QY	901	GGTGGTTTATATGCGACGCTCCCTGCAATGCTTATTTCTTTGAGCGTTGCAATTTG	960
Db	901	GGTGGTTTATATGCGACGCTCCCTGCAATGCTTATTTCTTTGAGCGTTGCAATTTG	960
QY	961	CTTGAGATCAACCGAGCGCAATATATCGCAATCTGGAATGTGTGCGTTGGCGACGTTG	1020
Db	961	CTTGAGATCAACCGAGCGCAATATATCGCAATCTGGAATGTGTGCGTTGGCGACGTTG	1020
QY	1021	ACACTCGTGCAATCTCTCAGAGACGGACCTCCGCTCGGTGACAGCAAGTGACGA	1080
Db	1021	ACACTCGTGCAATCTCTCAGAGACGGACCTCCGCTCGGTGACAGCAAGTGACGA	1080
QY	1081	TTTTTGGAAACACTCTGTTTACCGGCGGCAATGTTGTGTGCGGTGGGTTTGGCAATTACG	1140
Db	1081	TTTTTGGAAACACTCTGTTTACCGGCGGCAATGTTGTGTGCGGTGGGTTTGGCAATTACG	1140
QY	1141	CTTTCGGAATCTTCAGATGATATGTGCTGTGCAATGAGTCCGCTGACGACCTAATTA	1200
Db	1141	CTTTCGGAATCTTCAGATGATATGTGCTGTGCAATGAGTCCGCTGACGACCTAATTA	1200
QY	1201	TGCTCTACATTCGCCGCAATATATGCTGTGTGAGCTGACCGACGAGGCTTTGGCAGTGG	1260
Db	1201	TGCTCTACATTCGCCGCAATATATGCTGTGTGAGCTGACCGACGAGGCTTTGGCAGTGG	1260
QY	1261	TGTTACGGGAGTGGTCCCTCGGTGATTAATGCGGGGCTTAATCTGCGCTGATGGGTTCTGCG	1320
Db	1261	TGTTACGGGAGTGGTCCCTCGGTGATTAATGCGGGGCTTAATCTGCGCTGATGGGTTCTGCG	1320
QY	1321	TTTTATTAACCTTGCTGTTTATTTAATTAAGCCCGCTCTGCGCGCGCATTTGCTGCAACA	1380
Db	1321	TTTTATTAACCTTGCTGTTTATTTAATTAAGCCCGCTCTGCGCGCGCATTTGCTGCAACA	1380
QY	1381	GCAGTTGGTTTACATGCTGTGTGTTGCTTGCCGCTGCAATCTTGATTTCCACGTTAATGTG	1440
Db	1381	GCAGTTGGTTTACATGCTGTGTGTTGCTTGCCGCTGCAATCTTGATTTCCACGTTAATGTG	1440

QY	1441	GGGATTCGGCGCATCACACCAATGCTTCCAGGCTACCAATTTAACGGCGGAATGTACGCC	1500
Db	1441	GCGATTGCCCGGCAATCACACCAATGCTTCCAGGCTTACCAATTTAACGGCGGAATGTACGCC	1500
QY	1501	ACCGTGAATGATCAACACACTCATGGGTTTCAACCAACTTGGGTGGTTTAGCCACTGCT	1560
Db	1501	ACCGTGAATGATCAAAACACTCATGGGTTTCAACCAACTTGGGTGGTTTAGCCACTGCT	1560
QY	1561	TCATCACTTGGCGGTGGCGTGGTTTGGGTGATGGAATTGCGCGCAGGCTTACGTCTGCCA	1620
Db	1561	TCATCACTTGGCGGTGGCGTGGTTTGGGTGATGGAATTGCGCGCAGGCTTACGTCTGCCA	1620
QY	1621	CCAGGCTTCAACCCATACCGGTGATTTACCAAGCGAATGATGTTCTCTTCCAGAGAGAA	1680
Db	1621	CCAGGCTTCAACCCATACCGGTGATTTACCAAGCGAATGATGTTCTCTTCCAGAGAGAA	1680
QY	1681	GCTGAGCAGAATCGCGCGCGCAGAGAAAACGTCCAAAGACTAATTCAGAGATTGGGTAT	1740
Db	1681	GCTGAGCAGAATCGCGCGCGCAGAGAAAACGTCCAAAGACTAATTCAGAGATTGGGTAT	1740
QY	1741	AAAAGTAAAAAATCAACTGCTTGGGGGCTCTTGGCTTAAATAGCGAAGATATCGGGTC	1800
Db	1741	AAAAGTAAAAAATCAACTGCTTGGGGGCTCTTGGCTTAAATAGCGAAGATATCGGGTC	1800
QY	1801	GATGCGTTTTAAACACTCAGAGAGATCTTGGCGCGCAAAATTCACGGCACTCGTCCAC	1860
Db	1801	GATGCGTTTTAAACACTCAGAGAGATCTTGGCGCGCAAAATTCACGGCACTCGTCCAC	1860
QY	1861	CCCGAATATCCCTTCAGCGTGTGAAAGGAAACCGCAGCGCGGGATACCG	1909
Db	1861	CCCGAATATCCCTTCAGCGTGTGAAAGGAAACCGCAGCGCGGGATACCG	1909

```

RESULT 2
US-09-431-099-1
/ Sequence 1, Application US/09431099
/ Patent No. 6410705
/ GENERAL INFORMATION:
/ APPLICANT: Degussa-Höls AG
/ APPLICANT: Forschungszentrum-Joachim GmbH
/ TITLE OF INVENTION: New nucleotide sequences coding for the thre gene and process for
/ TITLE OF INVENTION: enzymatic production of L-threonine with coryneform bacteria.
/ FILE REFERENCE: 990079 BT
/ CURRENT APPLICATION NUMBER: US/09/431,099
/ CURRENT FILING DATE: 1999-11-01
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 2817
/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum ATCC14752
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (398)..(1864)
/ OTHER INFORMATION: thre-Gen
US-09-431-099-1

```

	Query Match	Similarity	Score	1336.6;	DB 4;	Length	2817;
	Best Local	Similarity	99.0%;	Pred.	NC. 0;	Mismatches	19;
	Matches	1848;	Conservative	0;	Mismatches	19;	Indels
							Gaps
							0
QY	38	CCCCCTTGAACCTGTGTTATTGAGCTGGAGAGAGACTTGAACCTCTCAACCTTACGCATTA	97				
Db	156	CCCCCTTGAACCTGTGTTATTGAGCTGGAGAGAGACTTGAACCTCTCAACCTTACGCATTA	215				
QY	98	CAAGTGCCTTGGGCGTCCCAATTGCCCACTCCAGACCGCGAGATGCTATGATCAACAAC	157				
Db	216	CAAGTGCCTTGGGCGTCCCAATTGCCCACTCCAGACCGCGAGATGCTATGATCAACAAC	275				
QY	158	TACGAAATACGATCTTGAAGCATGTGTATCATACAAATGAAATTCGGGGCTAGAGTATCTG	217				
Db	276	TACGAAATACGATCTTGAAGCATGTGTATCATACAAATGAAATTCGGGGCTAGAGTATCTG	335				

218 GTGAACCGTGATGAAAGCACTGTGATGGAATCTTTTCTTCCAAAATGTTTCCAGC 277
| | | | |
Db 336 GTGAACCGTGATGAAAGCACTGTGATGGAATCTTTTCTTCCAAAATGTTTCCAGC 395
| | | | |
Qy 278 GGATGTTGAGTTTGGCGACCCCTTGCTGGCCGCAATTTTCAACGTTGAGCTCCAAACCG 337
| | | | |
Db 396 GGATGTTGAGTTTGGCGACCCCTTGCTGGCCGCAATTTTCAACGTTGAGCTCCAAACCG 455
| | | | |
Qy 338 CACCTCCGCAATGCGCACTAGCCCGGATGATCTCAGTGAACATAGTCAAGTGGCCGATG 397
| | | | |
Db 456 CACCTCCGCAATGCGCACTAGCCCGGATGATCTCAGTGAACATAGTCAAGTGGCCGATG 515
| | | | |
Qy 398 TGATGAATTTGGCTGCGAAGATTGGCGAATTTTGGCTTTCTTCAGGTAAGTCAAAATAGT 457
| | | | |
Db 516 TGATGAATTTGGCTGCGAAGATTGGCGAATTTTGGCTTTCTTCAGGTAAGTCAAAATAGT 575
| | | | |
Qy 458 AACCAAGGTGCAAGTTCGAGCGGTGACCTGGGTGACGTTGGTACTTACACGACGTGG 517
| | | | |
Db 576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTGGGTGACGTTGGTACTTACACGACGTGG 635
| | | | |
Qy 518 ATATCAAGTGAATACGATCAACATCTTCAACCAATCGGTGAGAGAGAGAGATGCGCG 577
| | | | |
Db 636 ATATCAAGTGAATACGATCAACATCTTCAACCAATCGGTGAGAGAGAGAGATGCGCG 695
| | | | |
Qy 578 TCAACGTTTCAATGTTGAGGCAAGTTGGAACACCAATCTTCCAACTGTCTGAGGTTG 637
| | | | |
Db 696 TCAACGTTTCAATGTTGAGGCAAGTTGGAACACCAATCTTCCAACTGTCTGAGGTTG 755
| | | | |
Qy 638 ACCGTTGATCCGTTCCATTCAGGCTGGTGGAGCGCCGCTGAGGTGGCCGAGAAATCC 697
| | | | |
Db 756 ACCGTTGATCCGTTCCATTCAGGCTGGTGGAGCGCCGCTGAGGTGGCCGAGAAATCC 815
| | | | |
Qy 698 TGAACGATGAGCAATCCCTGCGCTCTATGAGTTTCCCTGTTGCGTTGCGTGGCG 757
| | | | |
Db 816 TGAACGATGAGCAATCCCTGCGCTCTATGAGTTTCCCTGTTGCGTTGCGTGGCG 875
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Qy 758 CAATGATGGTGTGCTGCTGTGCTGTGCTGTGAGTGGATGGCAGGTTTCCCTAATTG 817
| | | | |
Db 876 CAATGATGGTGTGCTGCTGTGCTGTGCTGTGAGTGGATGGCAGGTTTCCCTAATTG 935
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Qy 818 CTTTATTACCGGCTTACGATCATTTGCCAGCGATCTTTGGGAAAGAGGTTTGC 877
| | | | |
Db 936 CTTTATTACCGGCTTACGATCATTTGCCAGCGATCTTTGGGAAAGAGGTTTGC 995
| | | | |
Qy 878 CTACTTCTTCCAAAATGTTGTGTGTTTATTGCGACGCTGCTGCATCGATTCCTT 937
| | | | |
Db 996 CTACTTCTTCCAAAATGTTGTGTGTTTATTGCGACGCTGCTGCATCGATTCCTT 1055
| | | | |
Qy 938 ATTCTTTGGCGTTGCAATTTGCTTGAATCAAAACCGAGCCAGATCATGCAATCTGGAA 997
| | | | |
Db 1056 ATTCTTTGGCGTTGCAATTTGCTTGAATCAAAACCGAGCCAGATCATGCAATCTGGAA 1115
| | | | |
Qy 998 TTGTTGCTGTTGGGAGGTTTGAACCTGCTGCAATCTGCGAGAGCGGATCAACGCGCG 1057
| | | | |
Db 1116 TTGTTGCTGTTGGGAGGTTTGAACCTGCTGCAATCTGCGAGAGCGGATCAACGCGCG 1175
| | | | |
Qy 1058 CTCGCGTGAACGCAAGTGAACGATTTTTCGAAAACCTCTCGTTTACCGCGCGGATGTTG 1117
| | | | |
Db 1176 CTCGCGTGAACGCAAGTGAACGATTTTTCGAAAACCTCTCGTTTACCGCGCGGATGTTG 1235
| | | | |
Qy 1118 CTGGCGTGGGTTTGGGCAATTCAGCTTTCTGAATCTTTCGATGTCATGTTGCTGCCATGG 1177
| | | | |
Db 1236 CTGGCGTGGGTTTGGGCAATTCAGCTTTCTGAATCTTTCGATGTCATGTTGCTGCCATGG 1295
| | | | |
Qy 1178 AGTCGCTGAGACCAATTAATTGCTTACATTCGCGCGCAATTAATGCGGTGGGCTGA 1237
| | | | |
Db 1296 AGTCGCTGAGACCAATTAATTGCTTACATTCGCGCGCAATTAATGCGGTGGGCTGA 1355
| | | | |
Qy 1238 CCGCAGCGGCTTTCGAGTGGGTTGTTACGCGGAGTGGTCTCGATATTAATTCGCGGCG 1297
| | | | |
Db 1356 CCGCAGCGGCTTTCGAGTGGGTTGTTACGCGGAGTGGTCTCGATATTAATTCGCGGCG 1415
| | | | |

Qy 1298 TTAAGCGGTGATGAGGTTTTCGCTTTTATTAACTCTTGTGTTATTATAGCCCGCTCT 1357
| | | | |
Db 1416 TTAAGCGGTGATGAGGTTTTCGCTTTTATTAACTCTTGTGTTATTATAGCCCGCTCT 1475
| | | | |
Qy 1358 CTGCGCGTGGATTTGCTGCAACAGCAAGTGGTTTCACTGTTGTTTCTGCGCTGAT 1417
| | | | |
Db 1476 CTGCGCGTGGATTTGCTGCAACAGCAAGTGGTTTCACTGTTGTTTCTGCGCTGAT 1535
| | | | |
Qy 1418 TCTGATTTCCAGCTTATGTTGGCGATTTGCGCGCATCACACCAATGCTTCAGTCTAG 1477
| | | | |
Db 1536 TCTGATTTCCAGCTTATGTTGGCGATTTGCGCGCATCACACCAATGCTTCAGTCTAG 1595
| | | | |
Qy 1478 CAATTTACCGCGGATGTAAGCCCACTGATGATCAACCAATGATGATGATGATGATGAT 1537
| | | | |
Db 1596 CAATTTACCGCGGATGTAAGCCCACTGATGATCAACCAATGATGATGATGATGATGAT 1655
| | | | |
Qy 1538 TTGCGGTTGCTTTTACCACTGCTTCACTCTGCGCTGCGGTGTTTGGGTGATGGA 1597
| | | | |
Db 1656 TTGCGGTTGCTTTTACCACTGCTTCACTCTGCGCTGCGGTGTTTGGGTGATGGA 1715
| | | | |
Qy 1598 TTGCGCGCAGGCTAAGTGTGCAACCAAGCTTCAACCAATGATGATGATGATGATGATG 1657
| | | | |
Db 1716 TTGCGCGCAGGCTAAGTGTGCAACCAAGCTTCAACCAATGATGATGATGATGATGAT 1775
| | | | |
Qy 1658 ATGAGTTCTCTTCCAGAGAGAGCTGAGCAATACGCGCGCAGAGAAACGTCCAA 1717
| | | | |
Db 1776 ATGAGTTCTCTTCCAGAGAGAGCTGAGCAATACGCGCGCAGAGAAACGTCCAA 1835
| | | | |
Qy 1718 AGACTATCAAGATTTGCTTAAATTAAGTTAAATTAACCTGTTAGGCTCTTGTGCT 1777
| | | | |
Db 1836 AGACTATCAAGATTTGCTTAAATTAAGTTAAATTAACCTGTTAGGCTCTTGTGCT 1895
| | | | |
Qy 1778 TAAATAGCGTGAATATTCGGGTGATGCTTTTAAACATCTCAGAGAGATCTTGGCGGCG 1837
| | | | |
Db 1896 TAAATAGCGTGAATATTCGGGTGATGCTTTTAAACATCTCAGAGAGATCTTGGCGGCG 1955
| | | | |
Qy 1838 AAAATCAAGCACTGCTGCCACCCCAATCCCTTCAAGCTGTGTAAGAGAAACCGCA 1897
| | | | |
Db 1956 AAAATCAAGCACTGCTGCCACCCCAATCCCTTCAAGCTGTGTAAGAGAAACCGCA 2015
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Qy 1898 GCCGGGG 1904
| | | | |
Db 2016 GCCGGTG 2022
| | | | |

RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: PRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
Query Match 4.5%; Score 86.6; DB 3; Length 4403765;
Best Local Similarity 45.6%; Pred. No. 3; 4e-15;

Matches	498;	Conservative	0;	Mismatches	559;	Indels	36;	Gaps	4;
QY	531	TACGATCACCATTCTTCAACACATCGGTGTGAGAGAGAAAGTCCGGTCAACGTGTTCA							590
Db	4180213	TACGACATCATGTGTGTCGGCTAGGCAACACAGACATCCGCGGTACCATCATGCG							4180272
QY	591	TGTTGTAGGCAAGTTGACACACCACTTCTCAAACTGTCTGAGGTGACCGTTGATCCG							650
Db	4180273	GTGCGTCCGAGCCGCGTCACTGACTAGAGCCGGCTGGCCGACCTCGATGCACTGCTTCA							4180332
QY	651	TTCCATTACAGGCTGTGAGGACCCCGCTGAGGTTGCCAGAAATCTCGACGAGTTGGA							710
Db	4180333	GGGATTAACCTCCCGTGTGCGGTGAGTGCACAGGCTCAGAGGCTATGACGAGTTGAC							4180392
QY	711	GCAATCCCTGCTGTCTTATGTTTCCCTGTTGCTGCTGGTGGCAATGATGGTGG							770
Db	4180393	CGAAGCGGCCACCCCTACCCGCGCTGCGTCCGACCGCGGGGGGCGGCGCTTCGCACT							4180452
QY	771	TGCTGTGCTGTGCTGTGTTGGGTGTGATGGCAGGTTCCCTAATGCTTTATTAACCG							830
Db	4180453	CGGGGTGCGCATGTTGCTGGAGAACTGGCTGACCTGGCGTCTTGCGCTCGGACGTC							4180512
QY	831	GTTCACGATCATTTGCGACGAGTCAATTTTGGAAAGAGGATTTGCCATCTTCTTCA							890
Db	4180513	TGGCGTATTCACCGACCTGGGCGCGCTGCTGACCCGATCGGAAACCCGTTGTTCTCA							4180572
QY	891	AAATGTGTGTGTGTTTATTTATTCACGCTGCTGCATGATGTTTATCTTTGGCGTT							950
Db	4180573	GCGGCTGTGCGGCGGAGATCGACACCTGTGCTGCGGTGCGGTACTGATGCGCGG							4180632
QY	951	GCAATTTGTTGATGATCAACAGGACAGATCATCGCATCTGGAATGTTGTGCTGTT							1010
Db	4180633	CCA-----GGATTCGACCGCGTGGTGGCCACCGAATCGTTTGTGCTCT							4180677
QY	1011	GGCAGATTGACACTGCTGCAATCTCTGACAGACGACATCACGGCGCTCCGCTGACAGC							1070
Db	4180678	GTCTGGATGACCTGTGGGTGTGATGAGGACCGGCTACACCGGATACATGCTACCGC							4180737
QY	1071	AAGTGCAGATTTTTCGAAACACTCTCTGTTACCGGCGCATTTGTTGCTGGCGT							1124
Db	4180738	ACTGCGCGGCTGTGGCGAGCGCCCTGCTCTGACCGCAAGATCGCTGCGGATCTCAT							4180797
QY	1125	-----GGTTTGGGCACTTCAAGCTTTCGAAATCTTGATGATGATGCTGCTGCCAT							1175
Db	4180798	CTCGTTCGCGGCGCTACCAATATGCGGCAATCGAATGCAATGCAATGTCAGCAACAC							4180857
QY	1176	GGAATCCGCTGACGACCTAATTTATGCTAATTTGCTGCGGCAATTTATGCTGAGCGT							1235
Db	4180858	GACGCTGCCACCCCGGCGATGCGGCTACCGATTTCTGTCGGTAAAGGGTGGCGCT							4180917
QY	1236	CACGCGAGCGGCTTTCGAGTGGTGTGTTACCGGAGTGGTCTCGTATTTATGCGGG							1295
Db	4180918	GTCCGCGCTGTGCTGAGATGCGAGATGCGCGCTACGTTGTGCGCACCGCGG							4180977
QY	1296	GCTTACTG-----GATGAGGTTTTCGCTTATTAACCTTCGTTGTTATTTAGGCC							1352
Db	4180978	ACTCTGCGCGGACCTGCGCAACTGCTGCTATCGGACTGCGCGCGGGTGTGGCGG							4181037
QY	1353	CGTCTCTGCGCTGCGATTTGCTGCAACAGCAGTGTGTTCACTGTGTGTTGCTTCCCG							1412
Db	4181038	AGTGTGCGCACCTGACCGCGCGCATGCGGCTGCGCTTCTTGCGCACCTCATCTCAAT							4181097
QY	1413	TGATATTCTGATTTCAACGCTTATTTGAGGATTTGCGGATCAACAAATGCTTCCAGG							1472
Db	4181098	CCGTGCGAGGCTCCCGCTTGTGTGACGCGCACCGCGGATCATGCGATCTCCCGGG							4181157
QY	1473	TCTAGCAATTTACCGGGAATGTAGC---CACCTGATGATCAAAACATCATGAGTTT							1529
Db	4181158	CTTGTGCGTCTTCGTTGCGGTGTGCTGTGCGGTGCGGTATGACACACCGAGGGGTCT							4181217
QY	1530	CACCAACATTTGCGGTTGTTTATGACCATGCTTATCATCTTGGCGCTGGCGTGTGGG							1589
Db	4181218	GACCAAGCTGTGGAAGGGCGCGGACATGCACTGCGCTTGGCAGCGGGGTGTGTGGG							4181277

QY 1590 TGAATGATTTGCC 1602

Db 4181278 CGAGTTCTTCGCC 4181290

RESULT 4

US-09-103-840A-1

; Sequence 1, Application US/09103840A

; Patent No. 6294528

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103.840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

US-09-103-840A-1

Query Match 4.5%; Score 86.6; DB 3; Length 4411529;

Best Local Similarity 45.6%; Pred. No. 5.4e-15;

Matches 498; Conservative 0; Mismatches 559; Indels 36; Gaps 4;

QY	531	TACGATCACCATTCTTCAACACATCGGTGTGAGAGAGAAAGTCCGGTCAACGTGTTCA							590
Db	4187965	TACCAACATCATGTGTGTCGGCTAGGCAACACAGACATCCGCGGTACCATCATGCG							4188024
QY	591	TGTTGTAGGCAAGTTGACACACCACTTCCAACTGTCTGAGTTGACCGTTGATCCG							650
Db	4188025	GTGCGTCCGAGCCCGGTCTCACTGACTAAGCGCGGTGGCCGACCTGCATGACTGTTCA							4188084
QY	651	TTCCATTACAGGCTGTGAGGACCCCGCTGAGGTTGCCAGAAATCTCGACGAGTTGGA							710
Db	4188085	GCGGATACCTCCGGTGGCGTGCAGTGCACAGGCTCAGAGGCTATGAGCAAGTTGAC							4188144
QY	711	GCAATCCCTGCGTCTTATGTTTCCCTGTGCGTGTGCTGTGCTGGCAATGAGGTGG							770
Db	4188145	CGAAGCGGCCAACCCCTACCCGCGTGGCTGCGACCGCGGGGGCGGCGGCTTGCACT							4188204
QY	771	TGCTGTGCTGTGCTGTGAGGTTGATGAGGATTTCCCTAATTTGCTTTATTTACCGC							830
Db	4188205	CGGCTGCCCATGTTGCTGCGGGAACCTGCTGACCTGCGCTTGGCTGCCGTGACGTC							4188264
QY	831	GTTCACGATCATTTGCCACGACGTCAATTTTGGAAAGAGGTTTGCTTACTTTCTTCA							890
Db	4188265	TGGCGTATGACACGCACTGGCGCGCTGCTGAACCGGATTCGGGACCCCGTTGTTCTCA							4188324
QY	891	AAATTTTGTGTGTTTATTTGACAGCTGCTGCTGATGATGCTTATTTGTTGGCGTT							950
Db	4188325	GCGCGTTCGCGCGGAGATGCAACCTGTGTGCGGTGGCGGCTTACCTGATGCGCGG							4188384
QY	951	GCAATTTGTTGATGATCAACCGAGCGAGATCATTCGATCTGGAATGTTGTGCTGTT							1010
Db	4188385	CCA-----GGATTCGACCGCGCTGTGGTGGCACCGGAATGTTGTGTGCT							4188429
QY	1011	GGCAGTTTACACTGCTGCAATCTCTGAGAGAGGCAATCAAGCGCGCTCCGTTGACAGC							1070
Db	4188430	GTCTGGATGACCTTGTGTGTGCTGATGACGACCGGCTACACCGGATACATCTCACGCG							4188489
QY	1071	AAGTGCAGATTTTTCGAAACACTCTCTGTTTACCGGCGCATTTGTTGCTGGCGT							1124
Db	4188490	ACTGCGCGGCTGTGGAGCGCCCTGTTCTGACCGAGGATGCTGTGCGGATCTCAT							4188549

QY 1125 -----GGGTTGGGCAATTCAGCTTTCTGAATCTTGATGTCATGTTGCTGCCAT 1175
Db 4188550 CTCGTTGGGGGCGCTGACCAATGCGCGCATCCAGATCGAATCGATGCGACGACAC 4188609
QY 1176 GAGTCCGCTGACGACCACTTAATTTGCTTACATTTGCGCGCATTTATGCTGTGAGCT 1235
Db 4188610 GACCTGCGCACCCCGGCGATGCGCGCTACCAATTTCTGCGGGTGAAGCGGTGCGGCT 4188669
QY 1236 CACCGACAGCGGCTTTCGAGTGGGTTTTCACGCGAGTGTCTTCGATTAATTTGCGGG 1295
Db 4188670 GTCCGGGCTGTGCTGACGATCGAGCTATGCGCGCTAGCTTCTGTGCGCACCGCGG 4188729
QY 1296 GCTTACTGCG--GCTGATGGTTCTGCGTTTATTAATCTTCTGTTTATTTAGGCC 1352
Db 4188730 ACTCTGCGCGCGAGATTCGCGCACTGTGCTCATGCGACTCGCGCGCGGCTTCGCGG 4188789
QY 1353 CGTCTGCGCGCTGCGATGCTGCAACGAGTTGTTTCACTGCTGTGTTTGTCTGCGCG 1412
Db 4188790 AGTGTGCGCACTCGAAGCCGCGGATGCGGCTTCTTGGCCACCTGATTTCAAT 4188849
QY 1413 TCGATTTCTTAATTCACCGTTGATTTGCGGATTCGCGCATTCACCAATGCTTCAGG 1472
Db 4188850 CCGTCCGAGGCTCCCGCTTGTGAGGCGACCGCGCATTCATGCGATGCTGCGGG 4188909
QY 1473 TCTAGCAATTTACCGCGAATGTAGCG--CACCTGATGATTAACACTCATGCGTTT 1529
Db 4188910 CTTGCGGCTCTTCGTCGCGGTTCGCTGCGATGACACCGCGCGGCTCT 4188969
QY 1530 CACCAATTCGCGGTTCTTTAGCCACCTGCTTCACTTGC CGCGCGGCTTGGG 1589
Db 4188970 GACCCAGCTGCTGAGAGCGCGCGACTGCACTGCGCTTGGCAGCGGCGGTGGG 4189029
QY 1590 TGAATGATTCGCC 1602
Db 4189030 CGAGTTCCTCGCC 4189042

RESULT 5
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ19c-Fls
US-08-232-463-14
Query Match 2.5%; Score 47.6; DB 1; Length 7218;
Best Local Similarity 3.6%; Pred No. 0.000311;
Matches 14; Conservative 218; Mismatches 162; Indels 0; Gaps 0;
QY 1057 GCTCCGCTGACAGCAAGTGCAGATTTTTCGAAACCTCTGTTTACCGCGGCGATTGTT 1116
Db 1042 GCTCAGAGTGCAGGAGCTTGCGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1101
QY 1117 GCTGCGCTGGGTTGGGCAATTCAGCTTTGAAATCTTGATGATGATGCTGCGCATG 1176
Db 1102 TTT 1161
QY 1177 GAGTCCGCTGACAGCACTTAATTTGCTTACATTCGCGCGCATTCGCGGCTGCGGCTC 1236
Db 1162 TTT 1221
QY 1237 ACGCAGCGGCTTGCAGAGGTTGTACCGGAGTGTCTCGTATTAATTCGCGG 1296
Db 1222 TTT 1281
QY 1297 CTACGCGCTGATGGTTCTGCGTTTATTAATCTCTGCTGTTTATTAAGCCCGCTC 1356
Db 1282 TTT 1341
QY 1357 TCTGCGCTGCGATTCGTCGACAGCAGTTGTTTCACTGCTGCTGCTGCTGCTGCTG 1416
Db 1342 TTT 1401
QY 1417 TCTGATTCACCGTGTGATGCGGATTCGCG 1450
Db 1402 TTT 1435

RESULT 6
US-08-956-171E-4234/C
; Sequence 4234, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; APPLICANT: Gil H. Choi
; APPLICANT: Patrick S. Dillon
; APPLICANT: Craig A. Rosen
; APPLICANT: Steven C. Barash
; APPLICANT: Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4234:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4234:
US-08-956-171E-4234

Query Match 2.4% Score 46.6; DB 4; Length 400;
Best Local Similarity 61.9%; Pred. No. 9.8e-05;
Matches 73; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 32 ATCCCCCCTTGAAGCTGTTATTTAGCTGAGAGAGACTTGAACCTCAACTAC 91
Db 298 AGCCCAATCGTTACCCCTCAATATGTTGCGCGCCAGAGACTTGAAGCCCAACTAC 239
QY 92 GCATTACAGAGCGTTGGCTGCTCCCAATGCGGCACTCCAGACACCCCAATGCTGATGA 149
Db 238 TGATTACAGTCAGTGTCTTCAACCAATTGAGCTAGCGCGCTAAGAAATGTTACGGA 181

RESULT 7
US-09-198-452A-1
Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Grifffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention of infection and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (15001)-(30000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (30001)-(45000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (45001)-(60000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (60001)-(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (75001)-(90000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (90001)-(105000)
OTHER INFORMATION: n=a or c or g or t

LOCATION: (90001)-(105000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (105001)-(120000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (120001)-(135000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (135001)-(150000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (150001)-(165000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (165001)-(180000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (180001)-(195000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (195001)-(210000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (210001)-(225000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (225001)-(240000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (240001)-(255000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (255001)-(270000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (270001)-(285000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (285001)-(300000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (300001)-(315000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (315001)-(330000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (330001)-(345000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (345001)-(360000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (360001)-(375000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (375001)-(390000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (390001)-(405000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (405001)-(420000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (420001)-(435000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (435001)-(450000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (450001)-(465000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (465001)..(480000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (480001)..(495000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (495001)..(510000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (510001)..(525000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (525001)..(540000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (540001)..(555000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (555001)..(570000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (570001)..(585000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (585001)..(600000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (675001)..(690000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (690001)..(705000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (705001)..(720000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (720001)..(735000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (735001)..(750000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (750001)..(765000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (765001)..(780000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (780001)..(795000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (795001)..(810000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (810001)..(825000)
OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc feature
LOCATION: (825001)..(840000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (840001)..(855000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (855001)..(870000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature

Query Match 2.4%; Score 45.8; DB 4; Length 1230025;
Best Local Similarity 76.7%; Pred. No. 0.033;
Matches 56; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 61 GCTGAGAGAGACTTGAACCTCAACCTACGATTACAAGTGCCTGCGCAATTG 120
Db 303710 GCTGAGAGAGAGACTTGAACCTCAACCTGATTACAATGATGCTTGCATTG 303769
QY 121 CGCCACTCCAGCA 133
Db 303770 AGCTACTCCAGCA 303782

RESULT 8
US-08-956-171E-4023
Sequence 4023, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4023:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4023
US-08-956-171E-4023

Query Match
Best Local Similarity 73.1%; Pred. No. 0.0002;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

2.4%; Score 45.6; DB 4; Length 381;
Best Local Similarity 73.1%; Pred. No. 0.0002;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGGAGAGAGACTTGAACCTCTCAACCTACGATTACAGTGGCTGGCC 115
DB 87 ATGAGNGNGCCGAGAGACTTGAACCCCAACCTACTGATTACAGTCACTGCTTACC 146

QY 116 AATTGGCCCACTCCAGCA 133
DB 147 AATTGAGCTAGGCGCGCA 164

RESULT 9
US-08-956-171E-4566
Sequence 4566, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4566:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4566:
US-08-956-171E-4566

Query Match
Best Local Similarity 73.1%; Pred. No. 0.00036;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

2.3%; Score 44.4; DB 4; Length 237;
Best Local Similarity 73.1%; Pred. No. 0.00036;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGGAGAGAGACTTGAACCTCTCAACCTACGATTACAGTGGCTGGCC 115
DB 25 ATGTGTCGGCCGAGAGACTTGAACCCCAACCTACTGATTACAGTCACTGCTTACC 84

QY 116 AATTGGCCCACTCCAGCA 133
DB 85 AATTGAGCTAGGCGCGCA 102

RESULT 10
US-08-956-171E-4543
Sequence 4543, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4543:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4543:
US-08-956-171E-4543

Query Match
Best Local Similarity 73.1%; Pred. No. 0.00036;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

2.3%; Score 44.4; DB 4; Length 239;
Best Local Similarity 73.1%; Pred. No. 0.00036;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGGAGAGAGACTTGAACCTCTCAACCTACGATTACAGTGGCTGGCC 115
DB 81 ATGTGTCGGCCGAGAGACTTGAACCCCAACCTACTGATTACAGTCACTGCTTACC 140

QY 116 AATTGGCCCACTCCAGCA 133

Db 141 AATTGAGCTAGGCGCGCA 158

RESULT 11

US-08-956-171E-4544

; Sequence 4544, Application US/08956171E

; Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 4544:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

US-08-956-171E-4544

Query Match 2.3%; Score 44.4; DB 4; Length 239;

Best Local Similarity 73.1%; Pred. No. 0.00036;

Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 AATTGAGCTGAGAGAGACTTGAACCTCACTTACGATTAAGAAGTGGCGTGGC 115

DB 72 ATGTGCGCGCGCGAGAGACTTGAACCCCACTACTGATTCAAGTCAAGTGGCTCTACC 131

QY 116 AATTGGCGCACTCCAGCA 133

DB 132 AATTGAGCTAGGCGCGCA 149

RESULT 12

US-08-956-171E-3631

; Sequence 3631, Application US/08956171E

; Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 3631:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3631:

US-08-956-171E-3631

Query Match 2.3%; Score 44.4; DB 4; Length 400;

Best Local Similarity 73.1%; Pred. No. 0.0005;

Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 AATTGAGCTGAGAGAGACTTGAACCTCACTTACGATTAAGAAGTGGCGTGGC 115

DB 24 ATGTGCGCGCGCGAGAGACTTGAACCCCACTACTGATTCAAGTCAAGTGGCTCTACC 83

QY 116 AATTGGCGCACTCCAGCA 133

DB 84 AATTGAGCTAGGCGCGCA 101

RESULT 13

US-08-956-171E-3660

; Sequence 3660, Application US/08956171E

; Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 3660:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3660:
US-08-956-171E-3660

Query Match 2.3%; Score 44.4; DB 4; Length 400;
Best Local Similarity 73.1%; Pred. No. 0.0005;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGAGAGAGACTTGAACTCTCAACCTACGATTACAGAGTGGCTGCC 115
DB 20 ATGGTGGCGGCGAGAGCTTGAACTTGAACTTGATTAACAAGTGGCTGCC 79
QY 116 AATGGCGGCACTCCAGCA 133
DB 80 AATTGAGCTAGCGCGGCA 97

RESULT 14

US-08-956-171E-4198
Sequence 4198, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4198:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4198:
US-08-956-171E-4198

Query Match 2.3%; Score 44.4; DB 4; Length 400;
Best Local Similarity 73.1%; Pred. No. 0.0005;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 56 ATTGAGCTGAGAGAGACTTGAACTCTCAACCTACGATTACAGAGTGGCTGCC 115
DB 218 ATGGTGGCGGCGAGAGCTTGAACTTGAACTTGATTAACAAGTGGCTGCC 277
QY 116 AATGGCGGCACTCCAGCA 133
DB 278 AATTGAGCTAGCGCGGCA 295

RESULT 15

US-08-956-171E-4353
Sequence 4353, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789

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? REFERENCE/DOCKET NUMBER: PB248D1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (240) 314-1124
? TELEFAX: (301) 309-8439
? INFORMATION FOR SEQ ID NO: 4353:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 411 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 4353:
US-08-956-171E-4353

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Query Match	2.3%;	Score 44.4;	DB 4;	Length 411;
Best Local Similarity	73.1%;	Pred. No. 0.00051;		

Best Local Similarity	73.1%;	Pred. No. 0.00051;
Matches	57;	Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 56 ATTGAGCTGGAAAGATTTGAATCTCTCCTCACTTCCAGCTTCAACAATGGCTTCCGCTGCC 115
 Db 183 ATGTGCGCGGCGCAGAGACTTAACTCCCACTTACTGTATTCAGTCAAGTTGCTTACC 242
 OY 116 AATTGCGCAGCTCTCCAGCA 133
 Db 243 AATTGAGCTAGCGCGGCA 260

Search completed: July 31, 2004, 04:52:32Z
Job time : 148.915 secs

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QY 121 CGGCATCTCCGACACCGGAGATGCTGATGATCAACCACTAGAGATAGCTATCTTAGCTAT 180
DB 121 CGGCATCTCCGACACCGGAGATGCTGATGATCAACCACTAGAGATAGCTATCTTAGCTAT 180
QY 181 GTGTACATCACAATGGAATCGGGGCTAGAGTATCTGTGTAACCGTGCATTAAGACCTG 240
DB 181 GTGTACATCACAATGGAATCGGGGCTAGAGTATCTGTGTAACCGTGCATTAAGACCTG 240
QY 241 TGATTTGACCTTTTCTTCTTGCAAAATGTTTTCCAGCGGATGTGAGTTTGGCACTT 300
DB 241 TGATTTGACCTTTTCTTCTTGCAAAATGTTTTCCAGCGGATGTGAGTTTGGCACTT 300
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DB 301 CGTGGCCGCAATTTAAACAGTTGACGCTGCAAAAGCCGCACTCCGCAATGSCACTAGCC 360
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DB 361 CCGATTGATCTCACTGACCAATGATCAAGTGGCCGCTGTGATGAAATTTGGCTGCAAAAT 420
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DB 541 ATCTTCAACCAATCGGTGGAAGAGAAATGCCGTCAACGCTTCAATGTTGATGAGC 600
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DB 841 ATTGCGACGACGCTATTTTGGGAAAGAGGTTTGCCTACTTTCTCCAAATGTTGT 900
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DB 1141 CTTTTCGAAAATCTTGATGATGTTGCTGCGCATGAGATCCGCTCAGACCTAATAT 1200
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QY 1261 TGTTCGCGGAGTGTCTGCTGAGTATTAATGCGGAGCTTACTGCGCTGATGGTTCGCG 1320
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DB 1321 TTTTATTAACCTCTGCTGTTTATTTAGGCCCCGCTCTGCGCTGCGATGCTGCAACA 1380
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DB 1501 ACCCTGATGATCAACCAATGCTGATGAGTTTCAACCAATTTGCGTGTGCTTACCACTGCT 1560
QY 1561 TCATCACTTGGCGCTGCGGCTGAGTTTGGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1620
DB 1561 TCATCACTTGGCGCTGCGGCTGAGTTTGGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1620
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QY 1801 GATGCTTTTAAACACTCAGAGAGATCCTTGCAGGCGCAAAATCAAGCACTGTCGAC 1860
DB 1801 GATGCTTTTAAACACTCAGAGAGATCCTTGCAGGCGCAAAATCAAGCACTGTCGAC 1860
QY 1861 CCCAGATCCCTTCAAGCTGTTGAAGAGAAACCGCAGCCGCGGATACCG 1909
DB 1861 CCCAGATCCCTTCAAGCTGTTGAAGAGAAACCGCAGCCGCGGATACCG 1909

RESULT 2
US-09-963-521-3
; Sequence 3, Application US/09963521
; Patent No. US20020146781A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMAIC PRODUCTION OF
; TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/28243/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478-5
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3

LENGTH: 1909
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (280)..(1746)
OTHER INFORMATION: thrE-Gen
US-09-963-521-3

Query Match 100.0%; Score 1909; DB 9; Length 1909;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCTTGATGCTCTGAGTGTGATCTTGAGGATCCCCCTTTGACCTGCTGTTATGA 60
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Db 421 GCGGATATTTTCTTCTTCTGAGTACGTCATATAGTACACGAGGATCAAGTTCCAGCA 480
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QY 781 GTGCTGTTGGGTGGATGAGGATTTCCATATGCTTTTATTAACGCTTCAACGATC 840
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Db 841 ATTGCCACGAGCTCATTTTGGAGAAAGAGGTTGCTTACTTTCTTCCAAATGTTGT 900
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Db 1021 AACTGCTGCAATCTGCGAGAGACGCGATCAACGCGGCTCCGAGACAGCAAGTGCAGA 1080
QY 1081 TTTTTCGAAACACTCTGTTTACCGGCGGATTTGCTGCGCTGTTGGGCAATTCAG 1140
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QY 1141 CTTTCTGAATCTTGATGATGATGCTGCGATGAGATCCGCTGACGACCTAATAT 1200
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QY 1441 GCGATTCGCGGATCAACCAATGCTTCCAGTCTGACATTTTACCGCGGAAATGTAAGCC 1500
Db 1441 GCGATTCGCGGATCAACCAATGCTTCCAGTCTGACATTTTACCGCGGAAATGTAAGCC 1500
QY 1501 ACCCTGAATGATTAACATCTGATGCTTTCACCAATTTGCGGTTTACGCACTGCT 1560
Db 1501 ACCCTGAATGATTAACATCTGATGCTTTCACCAATTTGCGGTTTACGCACTGCT 1560
QY 1561 TCATCACTTGGCGCTGCGGCTGTTTGGGATGATGATGCGCGAGGCTACGCTGCTCA 1620
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Db 1801 GATCGCTTTTAAACACTGAGAGGATCTTTCGCGGCAAAATCAAGGACACTCGTCCAC 1860
QY 1861 CCGAGATCCCTTCAACGCTGTTGAAGAGAAACCGGAGCGGGGATACCG 1909
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RESULT 3
US-09-834-721-3
; Sequence 3, Application US/09834721
; Patent No. US2002015551A1

GENERAL INFORMATION:
APPLICANT: REBIP, MECHTILD
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
FILE REFERENCE: 21123/280169/MAS
CURRENT APPLICATION NUMBER: US/09/834,721
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: DE 100 26 494.8
PRIOR FILING DATE: 2000-05-27
PRIOR APPLICATION NUMBER: DE 101 02 823.7
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1909
TYPE: DNA
ORGANISM: *Corynebacterium glutamicum*
FEATURE:
OTHER INFORMATION: ATCC13032
NAME/KEY: CDS
LOCATION: (280)..(1746)
OTHER INFORMATION: thre gene
US-09-834-721-3

Query Match 100.0%; Score 1909; DB 9; Length 1909;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1081 TTTTTCGAAACACTCTGTTTACCGGCGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
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1621 CCAAGCTTCAACCCATACCGTGCATTTTCAAGGCAATGATTTCTCTTCCAGAGGAA 1680
1621 CCAAGCTTCAACCCATACCGTGCATTTTCAAGGCAATGATTTCTCTTCCAGAGGAA 1680
1681 GCTGAGCAGAAATCAACGCGCGGAGAGAAACCTTCAAAACATCAACGATTCGATTAAT 1740
1681 GCTGAGCAGAAATCAACGCGCGGAGAGAAACCTTCAAAACATCAACGATTCGATTAAT 1740
1681 GCTGAGCAGAAATCAACGCGCGGAGAGAAACCTTCAAAACATCAACGATTCGATTAAT 1740
1741 AAAAGTAAAAATCAACGCTGCTAGGCTTCTGCTTAAATAGGTAATATCGGCT 1800
1741 AAAAGTAAAAATCAACGCTGCTAGGCTTCTGCTTAAATAGGTAATATCGGCT 1800
1741 AAAAGTAAAAATCAACGCTGCTAGGCTTCTGCTTAAATAGGTAATATCGGCT 1800


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QY      1801 GATCGCTTTAAACACTCAGAGAGGATCCCTGCCGCGCAAAATACAGACACTCGTCCAC 1860
Db      1801 GATCGCTTTAAACACTCAGAGAGATCTTGCGCGCAAAATACAGACACTCGTCCAC 1860

QY      1861 CCCAGATCCCTTCACGCTGTGTGAAGAGGAAAACCGACGCGGAGTACC 1909
Db      1861 CCCAGATCCCTTCACGCTGTGTGAAGAGGAAAACCGACGCGGAGTACC 1909

RESULT 4
US-09-783-388-3      / Sequence 3, Application US/09783388
; Patent No. US2002016873A1
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Petra
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; APPLICANT: Thierbach, Georg
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR
; TITLE OF INVENTION: ENZYMAITC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/277066
; CURRENT APPLICATION NUMBER: US/09/783.388
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC13032
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
US-09-783-388-3

Query Match      100.0%; Score 1909; DB 9; Length 1909;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      AGCTTGCAATGCTCTGAGGTGCACTCTAGAGGATCCCCCCTTGTACCTGTATTATGA 60
Db      1      AGCTTGCAATGCTCTGAGGTGCACTCTAGAGGATCCCCCCTTGTACCTGTATTATGA 60

QY      61      GGTGAGAGAGAGACTTGAACCTCACTAGCACTTCAAGTGGTGGCGTGGCAATTG 120
Db      61      GGTGAGAGAGAGACTTGAACCTCACTAGCACTTCAAGTGGTGGCGTGGCAATTG 120

QY      121      CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTAGCAATAGCTATAGGCTAT 180
Db      121      CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTAGCAATAGCTATAGGCTAT 180

QY      181      GTGAACTCAAAATGGAATTTGGGGGCTTAGATATCTGTGAACCGTGCAATAACGACTG 240
Db      181      GTGAACTCAAAATGGAATTTGGGGGCTTAGATATCTGTGAACCGTGCAATAACGACTG 240

QY      241      TGATTGCACTCTTTTCTCTGCAAAATGTTTTCAGAGGATGTTGAGTGGACCTT 300
Db      241      TGATTGCACTCTTTTCTCTGCAAAATGTTTTCAGAGGATGTTGAGTGGACCTT 300

QY      301      CGTGGCGGCAATTTCAACAGTTGACGCTGCAAAAGCGCACCTCGGCATGCCACTAGCC 360
Db      301      CGTGGCGGCAATTTCAACAGTTGACGCTGCAAAAGCGCACCTCGGCATGCCACTAGCC 360

QY      361      CCGATTATCTCACTGACCACTAGCACTGCAAGTGGCGGCTGTGTAATTTGGCTGCAAAAT 420
Db      361      CCGATTATCTCACTGACCACTAGCACTGCAAGTGGCGGCTGTGTAATTTGGCTGCAAAAT 420

QY      421      GGGCATATTTTGGCTTCTTCAAGTACCTCAAAATAGTGAACCAAGGATCAAGTTGAGGA 480
Db      421      GGGCATATTTTGGCTTCTTCAAGTACCTCAAAATAGTGAACCAAGGATCAAGTTGAGGA 480

QY      481      GTGACCTTCGCGTAAGGCTTTGTACTACGACGAGTGGAATATCACTGTTGAATAGATCAC 540

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Db	481	GTGACCTCTGCGTACGGTTTGTACTACGACAGTGGATATCACTTGAATACGATCAC	540
QY	541	ATCTTACCAACATCGGTGTGAGAGGAAGATCCGGTCCACGTGTTTATGTGTAGGC	600
Db	541	ATCTTACCAACATCGGTGTGAGAGGAAGATCCGGTCAACGTGTTTATGTGTAGGC	600
QY	601	AAGTGGACACCACTTCTCCAACTGTGTAGAGTTGACCGTTTGATCCGTTCATTAG	660
Db	601	AAGTGGACACCAACTTCTCCAACTGTGTAGAGTTGACCGTTTGATCCGTTCATTAG	660
QY	661	GGTGGTGCACCCCGCTGAGTTGGCCGAGAAATCTGAGAGTTGGAGAAATCCCT	720
Db	661	GGTGGTGCACCCCGCTGAGTTGGCCGAGAAATCTGAGAGTTGGAGAAATCCCT	720
QY	721	GGGTCTTATGTTTCCCTGTTGCGTTGCTTGAGCTGGGCAATGATGGTGGTCTGTGCT	780
Db	721	GGGTCTTATGTTTCCCTGTTGCGTTGCTTGAGCTGGGCAATGATGGTGGTCTGTGCT	780
QY	781	GTGCTGTGGGTGGTGGATGGAGGTTTCCCTAATTTGCTTTATTTACGCGTTTCAGATC	840
Db	781	GTGCTGTGGGTGGTGGATGGAGGTTTCCCTAATTTGCTTTATTTACGCGTTTCAGATC	840
QY	841	ATTGCCACGACGTCAATTTTGGGAAAGAAAGGTTTGCCTACTTTCTTCCAAATGTGTT	900
Db	841	ATTGCCACGACGTCAATTTTGGGAAAGAAAGGTTTGCCTACTTTCTTCCAAATGTGTT	900
QY	901	GGTGGTTTATTTGCCACGCTGCGCTGCATCGATTCGTTATTTCTTGGCGTTGCAATTTGGT	960
Db	901	GGTGGTTTATTTGCCACGCTGCGCTGCATCGATTCGTTATTTCTTGGCGTTGCAATTTGGT	960
QY	961	CTTGGAGATCAAAACGAGCCAGATTCATCGCATCTGGAAATGTGTGTCGTGTTGGCAGTTTG	1020
Db	961	CTTGGAGATCAAAACGAGCCAGATTCATCGCATCTGGAAATGTGTGTCGTGTTGGCAGTTTG	1020
QY	1021	ACACTCTGTGCATCTCTTCCAGAGCGGATCAACGCGCGCTCCGGTACAGCAATGTACGA	1080
Db	1021	ACACTCTGTGCATCTCTCAGAGCGGATCAACGCGCGCTCCGGTACAGCAATGTACGA	1080
QY	1081	TTTTTCGAAACACTCTGTGTTTACGGGCGGCAATGTGTGTGGCGTGGGTTTGGGCAATTGAG	1140
Db	1081	TTTTTCGAAACACTCTGTGTTTACGGGCGGCAATGTGTGTGGCGTGGGTTTGGGCAATTGAG	1140
QY	1141	CTTTCGAAATCTTGCATGTGCATGTGTGGCTCCATGAGATCGCGCTGCAGCACTAATAT	1200
Db	1141	CTTTCGAAATCTTGCATGTGCATGTGTGGCTCCATGAGATCGCGCTGCAGCACTAATAT	1200
QY	1201	TGCTGTCAATTCGCGCCGATTAATGCGTGTGTGGCGGTCAACCGAGCGGCTTTGCAAGTGGGT	1260
Db	1201	TGCTGTCAATTCGCGCGATTAATGCGTGTGTGGCGGTCAACCGAGCGGCTTTGCAAGTGGGT	1260
QY	1261	TGTTACGGAGAGTGGTCTCTCGGATTAATTCGAGGGCTTACGTGCGATGAGTGTCTGCG	1320
Db	1261	TGTTACGGAGAGTGGTCTCTCGGATTAATTCGAGGGCTTACGTGCGATGAGTGTCTGCG	1320
QY	1321	TTTTTAATTAACCTCTTCTGTTGTTTATTTAGGCCCGCTCTGTGCGCTGCGATTCGTGCAACA	1380
Db	1321	TTTTTAATTAACCTCTTCTGTTGTTTATTTAGGCCCGCTCTGTGCGCTGCGATTCGTGCAACA	1380
QY	1381	GCAGTGGTGTTCATCTGAGGTTTGCTTGGCCGCTGATTTCTTGATTTCCACCGTTGATTTGTG	1440
Db	1381	GCAGTGGTGTTCATCTGAGGTTTGCTTGGCCGCTGATTTCTTGATTTCCACCGTTGATTTGTG	1440
QY	1441	GGCATTCGCGGATCAACAACATGCTTCCAGGCTTACGCAATTTACCGCGGAATGTACGCC	1500
Db	1441	GGCATTCGCGGATCAACAACATGCTTCCAGGCTTACGCAATTTACCGCGGAATGTACGCC	1500
QY	1501	ACCGTGAATGATCAAAACATCAATGAGGTTTACCAACATTCGTGGTGGTTTATGACCACTGCT	1560
Db	1501	ACCGTGAATGATCAAAACATCAATGAGGTTTACCAACATTCGTGGTGGTTTATGACCACTGCT	1560
QY	1561	TCATCACTTCCGCTGGCGTGGTTTGGATGAGTGAATTCGCGCAGGCTACGTCCTCA	1620

D _b	1561	TCATCACTGCGCGTGGCGGTGGTTTGGGTGAGTGGATTTGCCCGCAGACTACGTCTCCA	1620
Q _Y	1621	CCAAGCTTCAACCCATACCGTGCAATTTACCAAGCGCATGATGTTCTCTCTTCACAGAGAA	1680
D _b	1621	CCAGCGTTCAACCCATACCGTGCAATTTACCAAGCGCATGATGTTCTCTTCACAGAGAA	1680
Q _Y	1681	GCTAGCAGATTCAGCGCGCGGCACAGAAACGTCMAAGACTAATTCAGATTCGGTAT	1740
D _b	1681	GCTAGCAGATTCAGCGCGCGGCACAGAAACGTCMAAGACTAATTCAGATTCGGTAT	1740
Q _Y	1741	AAAAAGTAAAAATCAACTCTGTGAGGCGTCTTTGGCTTAATTAAGCTGATATTCGGGTC	1800
D _b	1741	AAAAAGTAAAAATCAACTCTGTGAGGCGTCTTTGGCTTAATTAAGCTGATATTCGGGTC	1800
Q _Y	1801	GATGCGTTTTAAACACTCAGAGAGATCTCTTCCGGCCAAATTCACGACACTCTGTCCAC	1860
D _b	1801	GATGCGTTTTAAACACTCAGAGAGATCTCTTCCGGCCAAATTCACGACACTCTGTCCAC	1860
Q _Y	1861	CCGAGATTCCTTCACTGCTGTTGAAGAGAAACCGCACCGGGGTATCCG	1909
D _b	1861	CCGAGATTCCTTCACTGCTGTTGAAGAGAAACCGCACCGGGGTATCCG	1909

RESULT 5

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US-09-951-535-3
; Sequence 3, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTMAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; TITLE OF INVENTION: USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282415/MAS
; CURRENT APPLICATION NUMBER: US/09/951,535
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
; OTHER INFORMATION: ltrE-Gen
US-09-951-535-3

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Query Match 100.0%; Score 1909; DB 10; Length 1909;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1909. Conservative 0: Mismatches 0: Indels 0: Gaps 0

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QY 1 AGCTTGACATCCCTGCAGAGTGGACTCTAGAGAGATCCCCCCTTTGACTGGTGTATTGA 60
 |||||
 Db 1 AGCTTGACATGCGCTGCAGAGTGGACTCTAGAGAGATCCCCCCTTTGACTGGTGTATTGA 60
 |||||
 QY 61 GCTGAGAGAGAGACTTGAACCTTCAACCTTACGATTTACAAGTGTGTTGGGCTGCCAATTG 120
 |||||
 Db 61 GCTGAGAGAGAGACTTGAACCTTCAACCTTACGATTTACAAGTGTGTTGGGCTGCCAATTG 120
 |||||
 QY 121 CGGCACCTCCAGCAGCCGCAAGTGTGATGATCAACCACTACGAAATGATCTTAGGCTAT 180
 |||||
 Db 121 CGGCACCTCCAGCAGCCGCAAGTGTGATGATCAACCACTACGAAATGATCTTAGGCTAT 180
 |||||
 QY 181 GTGTATATCAACATGGAATTCGGGGGCTAGAGTATCTGTGACCGGTGCATTAACGAACTTG 240
 |||||
 Db 181 GTGTATATCAACATGGAATTCGGGGGCTAGAGTATCTGTGACCGGTGCATTAACGAACTTG 240
 |||||

QY	241	TGATGGACCTCTTTTCTTCTTGCAAATATGTTTCCAAAGGATGTGAGTTTGCAACCCCT	300
Db	241	TGATTTGACCTCTTTTCTTCTTGCAAAATGTTTTCACAGGATGTGAGTTTGGACCCCT	300
QY	301	CGTGGCCGCAATTCAACAGTTGACGTGACGAAAAAGCCGCACTTCCGCATCGCACAAGCC	360
Db	301	CGTGGCCGCAATTCAACAGTTGACGTGACGAAAAAGCCGCACTTCCGCATCGCACAAGCC	360
QY	361	CCGATTGATCTCACTGACCAATAGTCAAGTGGCCGGTGTGTGTAATTTGGCTGGGAAATT	420
Db	361	CCGATTGATCTCACTGACCAATAGTCAAGTGGCCGGTGTGTGTAATTTGGCTGGGAAATT	420
QY	421	GGCAATATTTTGGCTTCTTGAGGAAGTCAAAATAGTACCAACAAGGTACAAGTTCCAGCA	480
Db	421	GGCAATATTTTGGCTTCTTGAGGAAGTCAAAATAGTACCAACAAGGTACAAGTTCCAGCA	480
QY	481	GTGACCTCTGCGATCGGTTTGTACTACAGCAGTGGATATCAAGTTGAATACATCAC	540
Db	481	GTGACCTCTGCGATCGGTTTGTACTACAGCAGTGGATATCAAGTTGAATACATCAC	540
QY	541	ATCTTACCAACATCGGTGTGGAGAAGAAATCCCGGTCAAGTGTTCATGTTATAGG	600
Db	541	ATCTTACCAACATCGGTGTGGAGAAGAAATCCCGGTCAAGTGTTCATGTTATAGG	600
QY	601	AAGTTGACACCAACTCTCCAACTGTCTGAGGTTGACCGTTGATCCGTTCCATTCA	660
Db	601	AAGTTGACACCAACTCTCCAACTGTCTGAGGTTGACCGTTGATCCGTTCCATTCA	660
QY	661	GCTGGTGCACCCCGCCTGAGGTTCGCCAGAAATCTGTGACAGATGGAGCAATCCCT	720
Db	661	GCTGGTGCACCCCGCCTGAGGTTCGCCAGAAATCTGTGACAGATGGAGCAATCCCT	720
QY	721	GCGTTTATGGTTCCCGTTCGCTTCTTGAGGCAATGATGGTGTGCTGTGCT	780
Db	721	GCGTTTATGGTTCCCGTTCGCTTCTTGAGGCAATGATGGTGTGCTGTGCT	780
QY	781	GTGCTGTGGGTGTGATGGCAGGTTTCCCTAATGCTTTTATTAACCGGTTTACATC	840
Db	781	GTGCTGTGGGTGTGATGGCAGGTTTCCCTAATGCTTTTATTAACCGGTTTACATC	840
QY	841	ATTGCAACAGCTCATTTTGGGAAAGAAGGTTTGCTACTTCTTCCAAATATGTTT	900
Db	841	ATTGCAACAGCTCATTTTGGGAAAGAAGGTTTGCTACTTCTTCCAAATATGTTT	900
QY	901	GGTGGTTTATGACACGCTCGCATATGCTTATTTCTTGGCGTTGCCAATTTGCT	960
Db	901	GGTGGTTTATGACACGCTCGCATATGCTTATTTCTTGGCGTTGCCAATTTGCT	960
QY	961	CTTGGAGATCAACCGAGCCAGATCATGCGATCTGGAATGTTGTGGTGGAGGTTG	1020
Db	961	CTTGGAGATCAACCGAGCCAGATCATGCGATCTGGAATGTTGTGGTGGAGGTTG	1020
QY	1021	ACACTGTGCAATCTCTGACAGACGGCATCAAGCGCGCTCCGATACACGAAGTGCAGA	1080
Db	1021	ACACTGTGCAATCTCTGACAGACGGCATCAAGCGCGCTCCGATACACGAAGTGCAGA	1080
QY	1081	TTTTTGGAAACATCTCTGTTTACCGCGCGCATTTGTTGTGGGTGGGTTTGGGATTCAG	1140
Db	1081	TTTTTGGAAACATCTCTGTTTACCGCGCGCATTTGTTGTGGGTGGGTTTGGGATTCAG	1140
QY	1141	CTTTCGAAATCTGTGATGTATGTTGTGCTGCGATGAGATCCGCTGCAGCACTTAATTAT	1200
Db	1141	CTTTCGAAATCTGTGATGTATGTTGTGCTGCGATGAGATCCGCTGCAGCACTTAATTAT	1200
QY	1201	TGCTCTACATTCGCCCGCATTTATGCTGTGTGCTGACCGACGCGCCTTGGCAATGGCT	1260
Db	1201	TGCTCTACATTCGCCCGCATTTATGCTGTGTGCTGACCGACGCGCCTTGGCAATGGCT	1260
QY	1261	TGTTTACGCGAGTGTCTCGGTGATTAATGGGAGGCTTACGCGCTAATGGCTCTGCG	1320
Db	1261	TGTTTACGCGAGTGTCTCGGTGATTAATGGGAGGCTTACGCGCTAATGGCTCTGCG	1320

QY 1321 TTTTATATCTCTTGGTGTGTTTATTTAGAGCCCCGCTCTGCGGCTGAGATTGCTGACAA 1380
 Db 1321 TTTTATATCTCTTGGTGTGTTTATTTAGAGCCCCGCTCTGCGGCTGAGATTGCTGACAA 1380
 QY 1381 GCAGTGTGTTTCACTGTGTGTGTTTGGTCCCGTGCATCTTGATTTCCACCGTGTATGTG 1440
 Db 1381 GCAGTGTGTTTCACTGTGTGTGTTTGGTCCCGTGCATCTTGATTTCCACCGTGTATGTG 1440
 QY 1441 GCGATTCGCGGATCAACCAATGCTTCAGAGTCTAGCAATTTAACCGGGAATGTAGCC 1500
 Db 1441 GCGATTCGCGGATCAACCAATGCTTCAGAGTCTAGCAATTTAACCGGGAATGTAGCC 1500
 QY 1501 ACCGTGATGATCAACCAATGCTTCAGCAAACTTGGGCTGTTTACCAACCTGCT 1560
 Db 1501 ACCGTGATGATCAACCAATGCTTCAGCAAACTTGGGCTGTTTACCAACCTGCT 1560
 QY 1561 TCATCACTTGGCGGTGGCGTGTGTTTGGTGTAGTGAATGGCCGAGCTACGTGCTCA 1620
 Db 1561 TCATCACTTGGCGGTGGCGTGTGTTTGGTGTAGTGAATGGCCGAGCTACGTGCTCA 1620
 QY 1621 CCAGCTTCAACCAATGCTTCAGTTTACCAAGGCGAATGATGTTCTCTTCCAGAGAA 1680
 Db 1621 CCAGCTTCAACCAATGCTTCAGTTTACCAAGGCGAATGATGTTCTCTTCCAGAGAA 1680
 QY 1681 GCTGAGCAGATCAGCGCGGAGAGAAAGTCCAAAGACTAATCAAGATTCGTAAT 1740
 Db 1681 GCTGAGCAGATCAGCGCGGAGAGAAAGTCCAAAGACTAATCAAGATTCGTAAT 1740
 QY 1741 AAAAGGTAATAATCAACTGCTTAAAGGCTTTCGTTAAATAGCTGTAATTCGGGTC 1800
 Db 1741 AAAAGGTAATAATCAACTGCTTAAAGGCTTTCGTTAAATAGCTGTAATTCGGGTC 1800
 QY 1801 GATCGCTTTTAAACCTCAGAGAGATCTTGGCGCAAAATCAAGCACTGTCAC 1860
 Db 1801 GATCGCTTTTAAACCTCAGAGAGATCTTGGCGCAAAATCAAGCACTGTCAC 1860
 QY 1861 CCCAGATCCCTTCAAGCTGTTGAAGAGAAACCGGCGGGTACCG 1909
 Db 1861 CCCAGATCCCTTCAAGCTGTTGAAGAGAAACCGGCGGGTACCG 1909

QY 61 GCTGAGAGAGACTTGAACCTCAACCTAGCAATTAACAAGTGGTGGCGTGCACAAATG 120
 Db 61 GCTGAGAGAGAGACTTGAACCTCAACCTAGCAATTAACAAGTGGTGGCGTGCACAAATG 120
 QY 121 CGCCATCTCAGACCGGAGATGCTGATGATCAACAATAACATAGTATAGCTAT 180
 Db 121 CGCCATCTCAGACCGGAGATGCTGATGATCAACAATAACATAGTATAGCTAT 180
 QY 181 GTGTGATCAACAATGAAATTCGGGCTAGAGTACTGATGAAACCGTGAATGAAGACTG 240
 Db 181 GTGTGATCAACAATGAAATTCGGGCTAGAGTACTGATGAAACCGTGAATGAAGACTG 240
 QY 241 TGATGAGACTTTTTCCTTGGCAAAATGTTTCCAGCGGATGTTGAGTTTGGACCTT 300
 Db 241 TGATGAGACTTTTTCCTTGGCAAAATGTTTCCAGCGGATGTTGAGTTTGGACCTT 300
 QY 301 CGTGCCGCAATTTCAACAGTTGACGCTGCAAAAGCCGACCTCCGCAATGCACTAGCC 360
 Db 301 CGTGCCGCAATTTCAACAGTTGACGCTGCAAAAGCCGACCTCCGCAATGCACTAGCC 360
 QY 361 CCGATTTGATCTCATGACATGATCAAGTGGCGGCTGATGAAATTTGGCTGCGAAT 420
 Db 361 CCGATTTGATCTCATGACATGATCAAGTGGCGGCTGATGAAATTTGGCTGCGAAT 420
 QY 421 GCGATATATTTGCTTTCCTTCAAGTACGCTCAATAGTACACCAAGGTACAAAGTTGAGCA 480
 Db 421 GCGATATATTTGCTTTCCTTCAAGTACGCTCAATAGTACACCAAGGTACAAAGTTGAGCA 480
 QY 481 GTGACCTCTGCGATGAGGTTTGTACTACAGCAGTGGATATCAAGTTGATGATGATACC 540
 Db 481 GTGACCTCTGCGATGAGGTTTGTACTACAGCAGTGGATATCAAGTTGATGATGATACC 540
 QY 541 ATCTTACCAACATGCGTGTGAGAGAGAAATGCGGCTCAAGTGTTCATGTTGAGGC 600
 Db 541 ATCTTACCAACATGCGTGTGAGAGAGAAATGCGGCTCAAGTGTTCATGTTGAGGC 600
 QY 601 AAGTTGAGACCAACTTCTCCAAACTGCTGAGGTTGACCGTTGATCCGTTCCATTCAG 660
 Db 601 AAGTTGAGACCAACTTCTCCAAACTGCTGAGGTTGACCGTTGATCCGTTCCATTCAG 660
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 QY 721 GCGCTTATGTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 Db 721 GCGCTTATGTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 781 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 Db 781 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 QY 841 ATTGCGACAGCTCATTTTGGGAAAGAGGTTTCCCTACTTCTTCCAAATGTTGT 900
 Db 841 ATTGCGACAGCTCATTTTGGGAAAGAGGTTTCCCTACTTCTTCCAAATGTTGT 900
 QY 901 GGTGTTTATTTTCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 Db 901 GGTGTTTATTTTCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 961 CTTGAGATCAACCGAGCGCAAGATCATGCTGATGAGATTGTTGCTGTTGGAGAGTTTG 1020
 Db 961 CTTGAGATCAACCGAGCGCAAGATCATGCTGATGAGATTGTTGCTGTTGGAGAGTTTG 1020
 QY 1021 ACACTGTGCAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 Db 1021 ACACTGTGCAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 QY 1081 TTTTTCGAAACACTCTCTGTTTACCGGCGGATTTGCTGCGCTGCTGCTGCTGCTGCTG 1140
 Db 1081 TTTTTCGAAACACTCTCTGTTTACCGGCGGATTTGCTGCGCTGCTGCTGCTGCTGCTG 1140

Query Match 100.0%; Score 1909; DB 17; Length 1909;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTGATGCTGAGAGTGAATCTAGAGATTCCTTGAACCTGATGTTATGA 60
 Db 1 AGCTTGATGCTGAGAGTGAATCTAGAGATTCCTTGAACCTGATGTTATGA 60

QY	1141	CTTTCGAAATCTTGACATGTCATGTTGCTGCGCATAGAGTCGCGCTGACAGCACTAATTAT	1200
Db	1141	CTTTCGAAATCTTGACATGTCATGTTGCTGCGCATAGAGTCGCGCTGACAGCACTAATTAT	1200
QY	1201	TGCGTCATATTCGCGCGGCATTTATTCGCGTGGAGGCGTACCGCAGCGGCTTCGAGTGGGT	1260
Db	1201	TGCGTCATATTCGCGCGGCATTTATTCGCGTGGAGGCGTACCGCAGCGGCTTCGAGTGGGT	1260
QY	1261	TGTTACGCGAGTGGTCCCTCGATGATTTATTCGCGGCTTACTGCGCTGATGSGTTCTGCG	1320
Db	1261	TGTTACGCGAGTGGTCCCTCGATGATTTATTCGCGGCTTACTGCGCTGATGSGTTCTGCG	1320
QY	1321	TTTTATTAACCTCTTCGTTGTTTATTTATGAGCCCGCTCTCTCCGCTGGGATTCGCAACA	1380
Db	1321	TTTTATTAACCTCTTCGTTGTTTATTTATGAGCCCGCTCTCTCCGCTGGGATTCGCAACA	1380
QY	1381	GCAGTGGGTTTCACTGGAGGTTTGCTTGCCCGTGGATTCTTGATTCACCGTTGATTTGTG	1440
Db	1381	GCAGTGGGTTTCACTGGAGGTTTGCTTGCCCGTGGATTCTTGATTCACCGTTGATTTGTG	1440
QY	1441	GCAGTTCGCGGCATCACACCAATGCTTTCAGAGTTCAGCAATTTACCGCGAATGTACGCC	1500
Db	1441	GCAGTTCGCGGCATCACACCAATGCTTTCAGAGTTCAGCAATTTACCGCGAATGTACGCC	1500
QY	1501	ACCCTGAATGATCAACAACATCATGAGGTTTTCACCAACATTTGGGTTGCTTTAGCCATGCT	1560
Db	1501	ACCCTGAATGATCAACAACATCATGAGGTTTTCACCAACATTTGGGTTGCTTTAGCCATGCT	1560
QY	1561	TCATCACTTCGCGCTGGCGGTGTTTGGGTGAGTGGATTTGCCCGCAGGCTACGTCGCA	1620
Db	1561	TCATCACTTCGCGCTGGCGGTGTTTGGGTGAGTGGATTTGCCCGCAGGCTACGTCGCA	1620
QY	1621	CCAGGCTTCAACCCATACCGTGCATTTTACCAAGCGAATGAGTTCTCTTCAGAGAGAA	1680
Db	1621	CCAGGCTTCAACCCATACCGTGCATTTTACCAAGCGAATGAGTTCTCTTCAGAGAGAA	1680
QY	1681	GCTGAGCAGATCAGCGCGCGCAGAGAAAAGCTCCAAAAGCTAATCAGAGTTGGTAT	1740
Db	1681	GCTGAGCAGATCAGCGCGCGCAGAGAAAAGCTCCAAAAGCTAATCAGAGTTGGTAT	1740
QY	1741	AAAAGTAAAAATCAACCTGCTTGGAGCGCTTTGGCTTAATGAGGTGATTCGAGT	1800
Db	1741	AAAAGTAAAAATCAACCTGCTTGGAGCGCTTTGGCTTAATGAGGTGATTCGAGT	1800
QY	1801	GATGCTTTTAAACACTCAGAGAGATCTTCGCGGCAGAAATCAGCACTGTCAC	1860
Db	1801	GATGCTTTTAAACACTCAGAGAGATCTTCGCGGCAGAAATCAGCACTGTCAC	1860
QY	1861	CCCAAGATCCCTTCAACGCTGTTGAAGAGAAAACCGCAGCCGGGATACG	1909
Db	1861	CCCAAGATCCCTTCAACGCTGTTGAAGAGAAAACCGCAGCCGGGATACG	1909
RESULT 7			
US-09-738-626-1			
; Sequence 1, Application US/09738626			
; Publication No. US20020197605A1			
GENERAL INFORMATION:			
; APPLICANT: NAKAGAWA, SATOSHI			
; APPLICANT: MIZOGUCHI, HIROSHI			
; APPLICANT: ANDO, SEIKO			
; APPLICANT: HAYASHI, MIKIRO			
; APPLICANT: OCHIAI, KEIKO			
; APPLICANT: YOKOI, HARUHIKO			
; APPLICANT: TATEISHI, NAOKO			
; APPLICANT: SENOH, AKIHIRO			
; APPLICANT: IKEDA, MASATO			
; APPLICANT: OZAKI, AKIO			
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES			
; FILE REFERENCE: 249-125			
; CURRENT APPLICATION NUMBER: US/09/738, 626			
; CURRENT FILING DATE: 2000-12-18			
; PRIOR APPLICATION NUMBER: JP 99/377484			

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? PRIOR FILING DATE: 1999-12-16
? PRIOR APPLICATION NUMBER: JP 00/159160
? PRIOR FILING DATE: 2000-04-07
? PRIOR APPLICATION NUMBER: JP 00/280398
? PRIOR FILING DATE: 2000-08-03
? NUMBER OF SEQ ID NOS: 7059
? SOFTWARE: PatentIn ver. 3.0
? SEQ ID NO 1
? LENGTH: 3309400
? TYPE: DNA
? ORGANISM: Corynebacterium glutamicum
? US-05-738-626-1

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Query Match	97.7%	Score 1865.4;	DB 9;	Length 3309400;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1866;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0

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QY 1118 CTGGCGTGGGTTTGGGCAATCAGCTTCTGAATCTTGAAATCTTGACATGTCATGCTGCGCATG 1177
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Db 2792600 GCGCGGG 2792606

RESULT 8
US-09-951-536-1
; Sequence 1, Application US/09951536
; Patent No. US20020107378A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGDELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERSCH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; FILE REFERENCE: 21123/282414/MAS
; CURRENT APPLICATION NUMBER: US/09/951,536
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398) ..(1864)
; OTHER INFORMATION: thre-Gen
US-09-951-536-1

Query Match 96.2%; Score 1836.6; DB 9; Length 2817;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1840; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Db 156 CCCCTTGACCTGCTGATTTAGCTGAGAGAAAGACTTAATCTTAACCTACGCTTA 215
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Db 636 AATACGTTGTAATACGATCACTTTTACCAACATGCGGTGAGAGAGATGCGG 695
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QY 578 TCAAGTGTTCATGTTGATGAGCAAGTTGGAACCAACTTCCAAAGCTGTGAGTTG 637
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Db 696 TCAAGTGTTCATGTTGATGAGCAAGTTGGAACCAACTTCCAAAGCTGTGAGTTG 755

QY 638 ACCGTTGATCGCTTCATTGAGGCTGTCGACACCCGCTGAGGTTCCGAGAAAATCC 697
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 QY 698 TGAACGAGTTGAGCAATCCCGCTGCGCTTATGAGTTTCCCTGTTGCGTTGCTGGG 757
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 QY 1238 CCGGAGCGGCTTCCGAGTGGTTGTACGCGAGTGTCTCTGAGTATTAATGCGAGG 1297
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 QY 1778 TAAATACGTAAGAAATATCGGCTGATGCTTTTAAACATCAGAGAGATCCTTGGCGG 1837
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 QY 1838 AAAATACGAGCACTGCTCCACCCAGAAATCCCTTACGCTGTTGAAGAAAACCGCA 1897
 DB 1956 AAAATACGAGCACTGCTCCACCCAGAAATCCCTTACGCTGTTGAAGAAAACCGCA 2015
 QY 1898 GCCGGGG 1904
 DB 2016 GCCGGTG 2022

RESULT 9
 US-09-963-521-1
 : Sequence 1, Application US/09963521
 : Patent No. US20020146781A1
 : GENERAL INFORMATION:
 : APPLICANT: ZIEGLER, PETRA
 : APPLICANT: EISELING, LOTHAR
 : APPLICANT: SAHM, HERMANN
 : TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE
 : TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
 : TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
 : FILE REFERENCE: 21123/282413/MAS
 : CURRENT APPLICATION NUMBER: US/09/963,521
 : PRIOR FILING DATE: 2001-09-27
 : PRIOR APPLICATION NUMBER: 09/431,099
 : PRIOR FILING DATE: 1999-11-01
 : PRIOR APPLICATION NUMBER: DE 199 41 478.5
 : NUMBER OF SEQ ID NOS: 10
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 1
 : LENGTH: 2817
 : TYPE: DNA
 : ORGANISM: Corynebacterium glutamicum
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (398)..(1864)
 : OTHER INFORMATION: three-Gen
 : US-09-963-521-1

Query Match 96.2%; Score 1836.6; DB 9; Length 2817;
 Best Local Similarity 99.0%; Pred. No. 0; Mismatches 19; Indels 0; Gaps 0;
 Matches 1848; Conservative

QY 38 CCCCTTACCTGCTGTTATTTAGCTGAGAGAAAGACTTGAACCTGCAACTAGCATTA 97
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 QY 158 TACGAATACGATCTTAGGATGATGATCATCAATGGAATTCGGGGCTAGATATCTG 217
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 QY 218 GTGAACCGTCAATAACGACCTGTGATTTGACTCTTTTCTTCTGCAAAATGTTTCCAG 277
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 DB 396 GGAATGATTTTGGGACCTTCTGTCGCGCATTTTCAACATTTACCGTGAAGGCG 455
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 DB 456 CACCTCCGCAATGCGACATGAGCCCGATGATCTCACTGACCAATGATCAAGTGGCGG 515

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Db 1596 CAATTTACCGGGAATGAGCCACCTGATGATCAACACATCATGAGTTTCAACA 1655
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QY 1898 GCCGCGG 1904
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Db 2016 GCCGCGG 2022
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RESULT 10
US-09-834-721-1
; Sequence 1, Application US/09834721
; Patent No. US2002015551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTILD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21133/280169/WAS
; CURRENT FILING DATE: US/09/834,721
; PRIOR FILING DATE: 2001-04-16
; PRIOR FILING DATE: 2000-05-27
; PRIOR FILING DATE: 2000-05-27
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC14752
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: three gene
US-09-834-721-1

Query Match 96.2%; Score 1836.6; DB 9; Length 2817;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 38 CCCCTTGAACCTGCGGTATTTAGCTGAGAAAGAACTTGAACCTCAACCTAAGCATTA 97
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Query Match 96.2%; Score 1836.6; DB 9; Length 2817;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 38 CCCCTTTGACCTGGTGTATTTAGCTGAGAGAGACTTGAACCTTCAACCTACGACTTA 97
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QY 158 TACGAATACGATCTTATGCGTATGTATGATCAATGAAATTCGGGGCTTATGATCTG 217
Db 276 TACGAATACGATCTTATGCGTATGTATGATCAATGAAATTCGGGGCTTATGATCTG 335

QY 218 GTGAACCGTGCATTAAGACCTGTGATTTGATCTTTCTTTGCAAAATGTTTCCAGC 277
Db 336 GTGAACCGTGCATTAAGACCTGTGATTTGATCTTTCTTTGCAAAATGTTTCCAGC 395

QY 278 GGATGTGAGTTTGGGACCTTGTGGCCGCAATTTCAACAGTTGACGCTGCAAAAGCCG 337
Db 396 GGATGTGAGTTTGGGACCTTGTGGCCGCAATTTCAACAGTTGACGCTGCAAAAGCCG 455

QY 338 CACCTCGGCAATGCGCACTAGCCCGCATTTGATCTCACTGACCAATGATCAAGTGGCGGTG 397
Db 456 CACCTCGGCAATGCGCACTAGCCCGCATTTGATCTCACTGACCAATGATCAAGTGGCGGTG 515

QY 398 TGAATGATTTGGCTGCGAGAAATGCGAATTTTGGCTTTCTTCAAGTACGTCGAATAGT 457
Db 516 TGAATGATTTGGCTGCGAGAAATGCGAATTTTGGCTTTCTTCAAGTACGTCGAATAGT 575

QY 458 AACCCAAAGTACAAAGTTTCAGACAGTAACTTTCGCTGATCGGTTTGTATCTACACGACGTG 517
Db 576 AACCCAAAGTACAAAGTTCAGACAGTAACTTTCGCTGATCGGTTTGTATCTACACGACGTG 635

QY 518 ATATCAGTTGAAATAGATCCATCTTACCAACATCGGTGTGGAGAGAGATCCCG 577
Db 636 ATATCAGTTGAAATAGATCCATCTTACCAACATCGGTGTGGAGAGAGATCCCG 695

QY 578 TCACCGTGTTCATGTTGAGCAAGTGGACACCAACTTCTCAAACTGTCTGAGGTTG 637
Db 696 TCACCGTGTTCATGTTGAGCAAGTGGACACCAACTTCTCAAACTGTCTGAGGTTG 755

QY 638 ACCGTTGATCCGTTCAATTCAGGCTGTGGCAACCCGCTGAGGTTGCCAGAAATCC 697
Db 756 ACCGTTGATCCGTTCAATTCAGGCTGTGGCAACCCGCTGAGGTTGCCAGAAATCC 815

QY 698 TGAACAGTTGAGCAATCCCTGCGCTTATGTTTCCCTGTTGCGTGTGCTGGG 757
Db 816 TGAACAGTTGAGCAATCCCTGCGCTTATGTTTCCCTGTTGCGTGTGCTGGG 875

QY 758 CAATAGGAGGTGTGCTGTGCTGTGCTGTGGGAGTGAATGAGAGGTTTCCCTAATTG 817
Db 876 CAATAGGAGGTGTGCTGTGCTGTGCTGTGGGAGTGAATGAGAGGTTTCCCTAATTG 935

QY 818 CTTTATTAACCGGCTTACGATCATTTGCCAGACGTCATTTTGGAAAGAGGTTTGC 877
Db 936 CTTTATTAACCGGCTTACGATCATTTGCCAGACGTCATTTTGGAAAGAGGTTTGC 995

QY 878 CTACTTCTTCCAAATGTTGTGAGTTTATTTGCAACGCTGCTGCATGATGATGCTT 937
Db 996 CTACTTCTTCCAAATGTTGTGAGTTTATTTGCAACGCTGCTGCATGATGATGCTT 1055

QY 938 ATTCTTGGCGTTCGAATTTGCTTGTGATCAAAACCGAGCAGATTCATGATCTGAA 997
Db 1056 ATTCTTGGCGTTCGAATTTGCTTGTGATCAAAACCGAGCAGATTCATGATCTGAA 1115

QY 998 TTGTTGCTGTGCGCAAGTTTGAACATCTGTGCAATCTTGTGAGAGACGCAATCACGGCG 1057
Db 1116 TTGTTGCTGTGCGCAAGTTTGAACATCTGTGCAATCTTGTGAGAGACGCAATCACGGCG 1175

QY 1058 CTCGGTGACAGCAAGTGCACGATTTTGAACAACCTCTGTTACCGCGCGCATGTTG 1117

Db 1176 CTCGGTGACAGCAAGTGCACGATTTTGAACAACCTCTGTTTACCGGCGCATGTTG 1235

QY 1118 CTGGCGTGGGTTTGGGATTCAGCTTTCGAAATCTTGCAATGTATGTCCTGCGCATG 1177

Db 1236 CTGGCGTGGGTTTGGGATTCAGCTTTCGAAATCTTGCAATGTATGTCCTGCGCATG 1295

QY 1178 AGTCCGTCAGACACCTTAATTATGCTCAATTCGCGGATTAATGCTGAGGCGCTCA 1237

Db 1296 AGTCCGTCAGACACCTTAATTATGCTCAATTCGCGGATTAATGCTGAGGCGCTCA 1355

QY 1238 CCGAGCGGCTTTCGAGAGTGGGTTTACGCGAGTGGTCCCTGAGTATTAATGCGGGGC 1297

Db 1356 CCGAGCGGCTTTCGAGAGTGGGTTTACGCGAGTGGTCCCTGAGTATTAATGCGGGGC 1415

QY 1298 TTACTGCGTGAATGGGTTCTGCGTTTATTAACCTTTCGTTGTTTATTAAGCCCGTCT 1357

Db 1416 TTACTGCGTGAATGGGTTCTGCGTTTATTAACCTTTCGTTGTTTATTAAGCCCGTCT 1475

QY 1358 CTGCGCTGCGATTTGCTGCAACAGAGTGGTTTCACTGAGTGGTTTCCCGCTGAT 1417

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QY 1418 TCTTGAATCCACGTTGATTTGTGGCGATTTGCCGCAATCAACCAATGCTTCCAGTCTAG 1477

Db 1536 TCTTGAATCCACGTTGATTTGTGGCGATTTGCCGCAATCAACCAATGCTTCCAGTCTAG 1595

QY 1478 CAATTTACCGCGGAATGTAAGCCACCTGATATGATCAACACTCATGAGGTTTCAACACA 1537

Db 1596 CAATTTACCGCGGAATGTAAGCCACCTGATATGATCAACACTCATGAGGTTTCAACACA 1655

QY 1538 TTGCGGTTCTTTAGGCACTGCTTCATCACTTGCCTGGCGGTGGTTTGGGAGTGGCA 1597

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Db 1716 TTGCCGAGGCTACGTCGTCCACACGCTTCAACCCATACCGTGTATTTACCAAGCGCA 1775

QY 1658 ATGAGTTCCTTCCAGAGGAAAGCTGACAGATATAGCGCGGCGAGAAACGTCGAA 1717

Db 1776 ATGAGTTCCTTCCAGAGGAAAGCTGACAGATATAGCGCGGCGAGAAACGTCGAA 1835

QY 1718 AGACTAATCAGAGATTCGCTTAATTAAGGTAAATCAACTGCTTAGCGCTTTCGCT 1777

Db 1836 AGACTAATCAGAGATTCGCTTAATTAAGGTAAATCAACTGCTTAGCGCTTTCGCT 1895

QY 1778 TAAATAGCTTAATATGCGGTGATGCTTTTAAACACTGAGAGGATCCTTGC CGGCC 1837

Db 1896 TAAATAGCTTAATATGCGGTGATGCTTTTAAACACTGAGAGGATCCTTGC CGGCC 1955

QY 1838 AAAATCAGGACACTGCTCCCAACCCAGAAATCCCTTCAAGCTGTGAAGAGAAACCGCA 1897

Db 1956 AAAATCAGGACACTGCTCCCAACCCAGAAATCCCTTCAAGCTGTGAAGAGAAACCGCA 2015

QY 1898 GCCGGGG 1904

Db 2016 GCCGGTG 2022

RESULT 12
US-09-951-535-1
; Sequence 1, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGBELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; FILE REFERENCE: 21123/282415/MAS

QY 1898 GCCGGGG 1904
Db 2016 GCCGGTG 2022

RESULT 13

US-10-224-574-9
; Sequence 9, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
; APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
; APPLICANT: P. Peters- Wendisch
; TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the syt
; TITLE OF INVENTION: L-Serin, improved process for the microbial manufacture of L-ser
; TITLE OF INVENTION: genetically modified microorganism suitable for the process.
; FILE REFERENCE: FZJ-9912-PCT
; CURRENT APPLICATION NUMBER: US/10/224,574
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: C. glutamicum ATCC 14 752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1867)
; OTHER INFORMATION: chr E (Threonin-exportcarrier)
US-10-224-574-9

Query Match 96.2%; Score 1836.6; DB 17; Length 2817;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 38 CCCCTTGAACCTGGTGTATTGAGCTGAGAGAGAGACTTGAACCTTCAACCTTACGCACTTA
Db 156 CCCCTTGAACCTGGTGTATTGAGCTGAGAGAGAGACTTGAACCTTCAACCTTACGCACTTA
QY 98 CAGATCGCTGGCGCTCCCAATTCGCGCATCTCCAGCACCGCAGATGCTGATGATCAACAC
Db 216 CAGATCGCTGGCGCTCCCAATTCGCGCATCTCCAGCACCGCAGATGCTGATGATCAACAC
QY 158 TAGAATACGTAATCTTAGAGGTATGTATACATCAATGGAATTCGGGGCTTAGATCTG 217
Db 276 TAGAATACGTAATCTTAGAGGTATGTATACATCAATGGAATTCGGGGCTTAGATCTG 335
QY 218 GTGAACCGTGATAACGACCTGTGATGAGACTCTTTTCTTGCAAAATGTTTCCAGC 277
Db 336 GTGAACCGTGATAACGACCTGTGATGAGACTCTTTTCTTGCAAAATGTTTCCAGC 395
QY 278 GGATGTGAGTTTGGAGACCTTCCTGCGCGCATTTCAACAGTTGACGCTGCAAAAAGCG 337
Db 396 GGATGTGAGTTTGGAGACCTTCCTGCGCGCATTTCAACAGTTGACGCTGCAAAAAGCG 455
QY 338 CACCTCCGCGCATCGCACCTAGCCCGATGATCTACCTGACATGTCGAATGGCCCGG 397
Db 456 CACCTCCGCGCATCGCACCTAGCCCGATGATCTACCTGACATGTCGAATGGCCCGG 515
QY 398 TGATGAATTTGGCTCGAGAAATTTGGAGATTTTCTTCTTCAGGTACGTCGAATAAG 457
Db 516 TGATGAATTTGGCTCGAGAAATTTGGAGATTTTCTTCTTCAGGTACGTCGAATAAG 575
QY 458 ACACCAAGGTACAATTTGGAGAGAGACCTTCGCGTACGTTTGAATCAACGACGCTGG 517
Db 576 ATACCAAGGTACAATTTGGAGAGAGACCTTCGCGTACGTTTGAATCAACGACGCTGG 635
QY 518 ATATCAAGGTACAATTTGGAGAGAGACCTTCACCAACATGAGTGGAGAGAGAGATCGCG 577
Db 636 ATATCAAGGTACAATTTGGAGAGAGACCTTCACCAACATGAGTGGAGAGAGAGATCGCG 695
QY 578 TCAACGTGTTCATGTTTGAAGCAAGTTGACACCACTTCCAACTGTCTGAGTTG 637
Db 696 TCAACGTGTTCATGTTTGAAGCAAGTTGACACCACTTCCAACTGTCTGAGTTG 755

QY 638 ACCGTTGATCCGTTCCATTGAGGCTGATGCGACCCCGCCGAGGTTCCCGAAGAAATCC 697
Db 756 ACCGTTGATCCGTTCCATTGAGGCTGATGCGACCCCGCCGAGGTTCCCGAAGAAATCC 815
QY 698 TGAACGATTTGAGCAATCCCTGCGCTTATGATTTCCCTGTTGCGGTTGCTGGCGG 757
Db 816 TGAACGATTTGAGCAATCCCTGCGCTTATGATTTCCCTGTTGCGGTTGCTGGCGG 875
QY 758 CAATGATGGGTGTGCTGTTGCTGCTGTGAGTGGATGGAGATGGCAGGTTCCCTAATG 817
Db 876 CAATGATGGGTGTGCTGTTGCTGCTGTGAGTGGATGGAGATGGCAGGTTCCCTAATG 935
QY 818 CTTTATTTACCGGTTGACATATTCGCGACAGCTATTTTGGAAAGAGGTTGCG 877
Db 936 CTTTATTTACCGGTTGACATATTCGCGACAGCTATTTTGGAAAGAGGTTGCG 995
QY 878 CTACTTCTTCAAAATGTTGTTGAGTGTATTTATGCGACGCTGCGCATGCTGCT 937
Db 996 CTACTTCTTCAAAATGTTGTTGAGTGTATTTATGCGACGCTGCGCATGCTGCT 1055
QY 938 ATTCTTTGGGCTTGCATTTGCTTGAATCAACCGAGCCAGATCATGCAATCTGAA 997
Db 1056 ATTCTTTGGGCTTGCATTTGCTTGAATCAACCGAGCCAGATCATGCAATCTGAA 1115
QY 998 TTGTTGCTGCTGGCAGGTTTGACACTGCTGGAATCTGCGAGAGCGCATCACGGGCG 1057
Db 1116 TTGTTGCTGCTGGCAGGTTTGACACTGCTGGAATCTGCGAGAGCGCATCACGGGCG 1175
QY 1058 CTCGGGTGACAGCAAGTGCACGATTTTTCGAAACACTCTGTTTACCGCGGCAATTGTT 1117
Db 1176 CTCGGGTGACAGCAAGTGCACGATTTTTCGAAACACTCTGTTTACCGCGGCAATTGTT 1235
QY 1118 CTGGCGGTGGTTTGGGCACTTACCTTCTGAATCTTGCAATGTCATGATGTTGCTGCAATG 1177
Db 1236 CTGGCGGTGGTTTGGGCACTTACCTTCTGAATCTTGCAATGTCATGATGTTGCTGCAATG 1295
QY 1178 AGTCGCTGACAGCACTTAATTTGCTACATTTGCGCGCATTAATGCGGTGGGTGCA 1237
Db 1296 AGTCGCTGACAGCACTTAATTTGCTACATTTGCGCGCATTAATGCGGTGGGTGCA 1355
QY 1238 CCGACGCGGCTTCCGAGTGGGTTGTTACCGGAGTGTCTCGGTATTAATGCGGGGCG 1297
Db 1356 CCGACGCGGCTTCCGAGTGGGTTGTTACCGGAGTGTCTCGGTATTAATGCGGGGCG 1415
QY 1298 TTACTGCGGTGATGGGTTCTGCTTTTATTAATCTCTGTTGTTATTTAGGCCCGGCT 1357
Db 1416 TTACTGCGGTGATGGGTTCTGCTTTTATTAATCTCTGTTGTTATTTAGGCCCGGCT 1475
QY 1358 CTGCGCTGCGATGCTGCAACAGAGTGGTTTCACTGAGTGGTTGCTTGGCCCGTGCAT 1417
Db 1476 CTGCGCTGCGATGCTGCAACAGAGTGGTTTCACTGAGTGGTTGCTTGGCCCGTGCAT 1535
QY 1418 TCTTATTTCAACCGTTGATGTTGGGATTCGCGGATCAACCAATGCTTCCAGGCTAG 1477
Db 1536 TCTTATTTCAACCGTTGATGTTGGGATTCGCGGATCAACCAATGCTTCCAGGCTAG 1595
QY 1478 CAATTTACCGGAGATGTAACCGCACCTGGAATGCAAAACATGATGGTTTCAACACA 1537
Db 1596 CAATTTACCGGAGATGTAACCGCACCTGGAATGCAAAACATGATGGTTTCAACACA 1655
QY 1538 TTGCGGTGCTTTAGCCACTGCTTCACTTTCGCGTGGCGTGGTTTGGGTGAGTGA 1597
Db 1656 TTGCGGTGCTTTAGCCACTGCTTCACTTTCGCGTGGCGTGGTTTGGGTGAGTGA 1715
QY 1598 TTGCGCGAGGCTACGCTGCTCAACCGCTTCAACCCATACCGTGAATTTACAGGCGA 1657
Db 1716 TTGCGCGAGGCTACGCTGCTCAACCGCTTCAACCCATACCGTGAATTTACAGGCGA 1775
QY 1658 ATGAGTTCTGCTTCAGAGGAGAGAGTGAAGATGAGCGCGCGCAGAGAAAGTGTCAA 1717
Db 1776 ATGAGTTCTGCTTCAGAGGAGAGAGTGAAGATGAGCGCGCGCAGAGAAAGTGTCAA 1835

QY 1718 AGACTATCAGAGATTGGTAAATAAAGGTAAATCAACTGCTTAAAGCGCTTTTCGCT 1777
 DB 1836 AGACTATCAAGATTGGTAAATAAAGGTAAATCAACTGCTTAAAGCGCTTTTCGCT 1895
 QY 1778 TAAATAGCGTAGAATATCGGCTGATCGCTTTAAACACTCAGAGAGATCCTTGGCCGCC 1837
 DB 1896 TAAATAGCGTAGAATATCGGCTGATCGCTTTAAACACTCAGAGAGATCCTTGGCCGCC 1955
 QY 1838 AAAATCAGGAGCACTGCTCCACCCGAGATCCCTTACGCTGTTGAAGAGAAACCGCA 1897
 DB 1956 AAAATCAGGAGCACTGCTCCACCCGAGATCCCTTACGCTGTTGAAGAGAAACCGCA 2015
 QY 1898 GCCGGGG 1904
 DB 2016 GCCGGTG 2022
 RESULT 14
 US-10-627-476-557
 ; Sequence 557, Application US/10627476
 ; Publication No. US2004030116A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Mark
 ; APPLICANT: Krogger, Burkhard
 ; APPLICANT: Schoder, Hartwig
 ; APPLICANT: Zeider, Oskar
 ; APPLICANT: Heberbauer, Gregor
 ; TITLE OF INVENTION: CORVNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
 ; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
 ; TITLE OF INVENTION: TRANSPORT
 ; FILE REFERENCE: BG1-125CPN
 ; CURRENT APPLICATION NUMBER: US/10/627,476
 ; PRIOR FILING DATE: 2003-07-25
 ; PRIOR APPLICATION NUMBER: 09/602,787
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: USSN 60/141031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: DE 19931454.3
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931478.0
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931563.9
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19932122.1
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932124.8
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932125.6
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932128.0
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932180.9
 ; PRIOR FILING DATE: 1999-07-09
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; Number of SEQ ID NOS: 678
 ; SEQ ID NO 557
 ; LENGTH: 1590
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (101)..(1567)
 ; OTHER INFORMATION: RXN00349
 ; US-10-627-476-557
 Query Match 83.3%; Score 1590; DB 13; Length 1590;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 180 TGTGTACATCAAGATGATTCGGGCTGAGATCTGTGTAACCGTGCATTAAGGACT 239
 DB 1 TGTGTACATCAAGATGATTCGGGCTGAGATCTGTGTAACCGTGCATTAAGGACT 60

QY 240 GTGATTGACCTCTTTTCTTGGAAAAATSTTTTCCAGCGAGATGTGAGTTTTCGACCT 299
 DB 61 GTGATTGACCTCTTTTCTTGGAAAAATSTTTTCCAGCGAGATGTGAGTTTTCGACCT 120
 QY 300 TGTGGCCGCAATTTCAACAGTTGAGCGCTGCAAAAGCCGCACTCCGCCATCGCAGTAC 359
 DB 121 TGTGGCCGCAATTTCAACAGTTGAGCGCTGCAAAAGCCGCACTCCGCCATCGCAGTAC 180
 QY 360 CCCGATGATTCACAGCAATGATGATGAGCGCGGATGATGATTTGGCTCGAGAAAT 419
 DB 181 CCCGATGATTCACAGCAATGATGATGAGCGCGGATGATGATTTGGCTCGAGAAAT 240
 QY 420 TGGCGATATTTGCTTCTTCAAGTACGTCAAAATAGTACACCAAGTACAAAGTTGAGC 479
 DB 241 TGGCGATATTTGCTTCTTCAAGTACGTCAAAATAGTACACCAAGTACAAAGTTGAGC 300
 QY 480 AGTACCTTGGCGTAGCGTTTGTACTACAGCAGCTGAGATATACAGTTGAATACGATCAC 539
 DB 301 AGTACCTTGGCGTAGCGTTTGTACTACAGCAGCTGAGATATACAGTTGAATACGATCAC 360
 QY 540 CATCTTCAACCAATGATGATGAGAGAGAAATGCGGTCACAGTGTTCATGTTGAGG 599
 DB 361 CATCTTCAACCAATGATGATGAGAGAGAAATGCGGTCACAGTGTTCATGTTGAGG 420
 QY 600 CAAGTTGACACCAACTTCTCCAACTGTCTGAGTTGACCGTTGATCCGTTCAATCA 639
 DB 421 CAAGTTGACACCAACTTCTCCAACTGTCTGAGTTGACCGTTGATCCGTTCAATCA 480
 QY 660 GGTGTGTCGACCCCGCTGAGTTGCGGAGAAATCTGTGACAGATTTGAGAGCAATCCC 719
 DB 481 GGTGTGTCGACCCCGCTGAGTTGCGGAGAAATCTGTGACAGATTTGAGAGCAATCCC 540
 QY 720 TGGCTTATGATTTTCCCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
 DB 541 TGGCTTATGATTTTCCCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 780 TGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 839
 DB 601 TGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 840 CATTGCCAGCAGCTATTTTGGGAAAGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
 DB 661 CATTGCCAGCAGCTATTTTGGGAAAGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 900 TGTGCTGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959
 DB 721 TGTGCTGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 960 TCTTGATCAAAACGAGCCAGATCATGATGATGATGATGATGATGATGATGATGATGAT 1019
 DB 781 TCTTGATCAAAACGAGCCAGATCATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 1020 GACACTGCTGATTCCTGAGAGAGAGGATCAGAGGAGCTCCGAGTGAAGAGAGAGAG 1079
 DB 841 GACACTGCTGATTCCTGAGAGAGAGGATCAGAGGAGCTCCGAGTGAAGAGAGAGAG 900
 QY 1080 ATTTTGGAAACACTCTGTTTACCGCGGCAATTTGCTGCGGTGAGGATTTCA 1139
 DB 901 ATTTTGGAAACACTCTGTTTACCGCGGCAATTTGCTGCGGTGAGGATTTCA 960
 QY 1140 GCTTCTGAATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1199
 DB 961 GCTTCTGAATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 QY 1200 TTTGCTACATTCGCGCGGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1259
 DB 1021 TTTGCTACATTCGCGCGGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 QY 1260 TTTGCTACGAGAGATGCTCTGCTGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1319
 DB 1081 TTTGCTACGAGAGATGCTCTGCTGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 QY 1320 GTTTTATTAACCTTCTGCTGTTTATTTAGGCGCCGCTCTGCGCGTGGATTTGCTCAAC 1379

Db 1141 GTTTATTACCTCTTCGTTGTTTATTAGAGCCCGCTCTGCGCGTGAGATTGCTGAAAC 1200
QY 1380 AGCAGTTGGTTTCACTGGTGGTTTGGTGGCCGTCGATTTCTTGATTCACCGTTGATTGT 1439
Db 1201 AGCAGTTGGTTTCACTGGTGGTTTGGTGGCCGTCGATTTCTTGATTCACCGTTGATTGT 1260
QY 1440 GGGCATTGGCCGGGATTCACCAATGCTTCCAGTCTTGAGCAATTTTACCGCGAATGTAAGC 1499
Db 1261 GGGCATTGGCCGGGATTCACCAATGCTTCCAGTCTTGAGCAATTTTACCGCGAATGTAAGC 1320
QY 1500 CACCTGAATGATCAACATCACTCATGGGTTTCCAAACATTTGGGTTTCTTATGCACTGC 1559
Db 1321 CACCTGAATGATCAACATCACTCATGGGTTTCCAAACATTTGGGTTTCTTATGCACTGC 1380
QY 1560 TTTCATCACTTGGCCGCTGGCTGGTGGTTTGGTGGATGATGCGCGAGGCTACGTCGTC 1619
Db 1381 TTTCATCACTTGGCCGCTGGCTGGTGGTTTGGTGGATGATGCGCGAGGCTACGTCGTC 1440
QY 1620 ACCACGCTTCAACCCCAATACCGTGTATTTTACCAAGCGCAATGATTTCTTCCAGAGGA 1679
Db 1441 ACCACGCTTCAACCCCAATACCGTGTATTTTACCAAGCGCAATGATTTCTTCCAGAGGA 1500
QY 1680 AGCTGAGCAGATTCAGCGCGCGAGAGAAACGTCGAAGCTTATGAGATTTCCGTTAA 1739
Db 1501 AGCTGAGCAGATTCAGCGCGCGAGAGAAACGTCGAAGCTTATGAGATTTCCGTTAA 1560
QY 1740 TAAAGGTAAATCAACCTGCTTAGGCGT 1769
Db 1561 TAAAGGTAAATCAACCTGCTTAGGCGT 1590

RESULT 15
US-10-450-055-41
/ Sequence 41, Application US/10450055
/ Publication No. US20040043953A1
/ GENERAL INFORMATION:
/ APPLICANT: BASF Aktiengesellschaft
/ TITLE OF INVENTION: No. US20040043953A1 genes of *Corynebacterium*
/ FILE REFERENCE: 936, 2000
/ CURRENT APPLICATION NUMBER: US/10/450,055
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: PatentIn Vers. 2.0
/ SEQ ID NO 41
/ LENGTH: 1590
/ TYPE: DNA
/ ORGANISM: *Corynebacterium glutamicum*
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (101)..(1567)
/ OTHER INFORMATION: RKS00349
US-10-450-055-41

Query Match 83.3%; Score 1590; DB 13; Length 1590;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 TGTGTACATCAACATGGAATTCGCGGCTAGAGTATCTGTGAACCGTGCATTAACGACCT 239
Db 1 TGTGTACATCAACATGGAATTCGCGGCTAGAGTATCTGTGAACCGTGCATTAACGACCT 60
QY 240 GGTATTTGACCTCTTTTCTTGGCAAAATTTTCCAGCGGATGTTGAGTTTTCGACCT 299
Db 61 GGTATTTGACCTCTTTTCTTGGCAAAATTTTCCAGCGGATGTTGAGTTTTCGACCT 120
QY 300 TGTGTGCGCATTTTCAACAGTTGACGCTGCAAAAGCGGACCTCGGCACTGGCCACTAGC 359
Db 121 TGTGTGCGCATTTTCAACAGTTGACGCTGCAAAAGCGGACCTCGGCACTGGCCACTAGC 180
QY 360 CCGGATGATCTCACTGACCAATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCAGAAAT 419
Db 181 CCGGATGATCTCACTGACCAATAGTCAAGTGGCCGGTGTGATGAATTTGGCTGCAGAAAT 240

QY 420 TGGCATATTTTGGTTTCTTCAAGTACGTCGCAATAGTACCAAGGTAACAAGTTGAGC 479
Db 241 TGGCATATTTTGGTTTCTTCAAGTACGTCGCAATAGTACCAAGGTAACAAGTTGAGC 300
QY 480 AGTACCTGTCGTCAGGTTTGTACTACAGCAAGTGGATGATCACTTGAATAGATCAC 539
Db 301 AGTACCTGTCGTCAGGTTTGTACTACAGCAAGTGGATGATCACTTGAATAGATCAC 360
QY 540 CATTTTCAACCAATCGGTGTGAGAGGAAGATGCGGTCGACGTTTCAATGTTGAG 599
Db 361 CATTTTCAACCAATCGGTGTGAGAGGAAGATGCGGTCGACGTTTCAATGTTGAG 420
QY 600 CAAGTTGACACCAACCTTCCAACTGTCGAGGTTGACCGTTTGAATCCGTTCAATCA 659
Db 421 CAAGTTGACACCAACCTTCCAACTGTCGAGGTTGACCGTTTGAATCCGTTCAATCA 480
QY 660 GGTGTGTGCGACCCCGCTGAGGTTGCGGAGAAATCTGTGAGAGTGGAGCAATCCC 719
Db 481 GGTGTGTGCGACCCCGCTGAGGTTGCGGAGAAATCTGTGAGAGTGGAGCAATCCC 540
QY 720 TGGCTTATAGTTTCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 779
Db 541 TGGCTTATAGTTTCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 600
QY 780 TGTGCTGTGGGTGATGATGAGGTTTCCATATGCTTTTATTAACCGCGTTCAAGAT 839
Db 601 TGTGCTGTGGGTGATGATGAGGTTTCCATATGCTTTTATTAACCGCGTTCAAGAT 660
QY 840 CATTTGCAACGACGTCATTTTGGGAAAGAGGTTTGCCTACTTCTTCCAAATGTTGT 899
Db 661 CATTTGCAACGACGTCATTTTGGGAAAGAGGTTTGCCTACTTCTTCCAAATGTTGT 720
QY 900 TGGTGTGTTTATTTGCCACGCTGCTGTCGATGATGCTTATTTTGGCGTTGCAATTTGG 959
Db 721 TGGTGTGTTTATTTGCCACGCTGCTGTCGATGATGCTTATTTTGGCGTTGCAATTTGG 780
QY 960 TCTTGTGATCAAAACGAGCCAGATCATGCAATGGAATTTGTGTGCTGTGCGAGTTT 1019
Db 781 TCTTGTGATCAAAACGAGCCAGATCATGCAATGGAATTTGTGTGCTGTGCGAGTTT 840
QY 1020 GACACTGTGCAATCTTCCAGAGCGGATCAACGCGCGCTCCGCTGACAGCAATGTCAGC 1079
Db 841 GACACTGTGCAATCTTCCAGAGCGGATCAACGCGCGCTCCGCTGACAGCAATGTCAGC 900
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 31, 2004, 09:27:29 ; Search time 1068 Seconds

(without alignments)
143,624 Million cell updates/sec

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2432	100.0	489	US-09-951-536-4	Sequence 4, Appli
3	2432	100.0	489	US-09-963-521-2	Sequence 2, Appli
4	2432	100.0	489	US-09-963-521-4	Sequence 4, Appli
5	2432	100.0	489	US-09-834-721-2	Sequence 2, Appli
6	2432	100.0	489	US-09-834-721-4	Sequence 4, Appli
7	2432	100.0	489	US-09-783-388-2	Sequence 2, Appli
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10	2432	100.0	489	US-09-951-535-4	Sequence 4, Appli
11	2432	100.0	489	US-10-627-476-558	Sequence 558, App
12	2432	100.0	489	US-10-450-055-42	Sequence 42, Appli
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45	124.5	5.1	419	12	US-10-282-1222A-59807	Sequence 59807, A

ALIGNMENTS

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RESULT 1
US-09-951-536-2
; Sequence 2, Application US/09951536
; Patent No. US20020107378A1
GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTMAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; TITLE OF INVENTION: USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282414/MAS
; CURRENT APPLICATION NUMBER: US/09/951,536
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-951-536-2

Query Match      100.0%; Score 2432; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.56-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 4, Application US/09951536
; Patent No. US20020107378A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTMAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THERERACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; TITLE OF INVENTION: USING CORNEFORM BACTERIA
; FILE REFERENCE: 21123/282414/MAS
; CURRENT APPLICATION NUMBER: US/09/951,536
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 489
; TYPE: PRF
; ORGANISM: Corynebacterium glutamicum
US-09-951-536-4

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RESULT 3
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; Patent No. US20020146781A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTMAR
; APPLICANT: SAHM, HERMANN
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
; TITLE OF INVENTION: L-THREONINE USING CORNEFORM BACTERIA
; FILE REFERENCE: 21123/282413/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 489
; TYPE: PRF
; ORGANISM: Corynebacterium glutamicum
US-09-963-521-2

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; Patent No. US20020146781A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTMAR
; APPLICANT: SAMM, HERMANN
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMAATIC PRODUCTION OF
; TITLE OF INVENTION: L-THREONINE USING CORINEFORM BACTERIA
; FILE REFERENCE: 21123/282413/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-963-521-4

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Best Local Similarity 100.0%; Pred. No. 4.5e-214;
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RESULT 5

US-09-834-721-2
; Sequence 2, Application US/09834721
; Patent No. US2002015551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21123/280169/MAS
; CURRENT APPLICATION NUMBER: US/09/834,721
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: DE 100 26 494.8
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: DE 101 02 823.7
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC14752
US-09-834-721-2

Query Match 100.0%; Score 2432; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 RLIRSIQAGATPEPEAEKILDELBOSSPASXGFPVALLGAMMGGAVALILGGMWVSILA 180
QY 181 FITAFTIATTSFLGKGLPTFFQNVVGGFIATLPASIAVSLALQGLIERSQIIASGI 240
Db 181 FITAFTIATTSFLGKGLPTFFQNVVGGFIATLPASIAVSLALQGLIERSQIIASGI 240
QY 241 VVLAAGLTLVOSLQDGTIGAPVTASARPEFTLLFTGGIVAGVGLGIQSEILHVMLPAME 300
Db 241 VVLAAGLTLVOSLQDGTIGAPVTASARPEFTLLFTGGIVAGVGLGIQSEILHVMLPAME 300
QY 301 SAAAPNYSSTFARIIAGVTAAAFVAGVCAEMSSVIIAGLTALMGSAFYVLFVYVLGYS 360
Db 301 SAAAPNYSSTFARIIAGVTAAAFVAGVCAEMSSVIIAGLTALMGSAFYVLFVYVLGYS 360
QY 361 AAAIATAVAGFTGGLIARRFLIPPLIYAIAGITPMLPGAIYRGMYATLNDQTLMGFTNI 420
Db 361 AAAIATAVAGFTGGLIARRFLIPPLIYAIAGITPMLPGAIYRGMYATLNDQTLMGFTNI 420
QY 421 AVAALATASSIAAGVIGEMIARLRPPRPYRAFTKANEFSFOEAEONQRORRKP 480
Db 421 AVAALATASSIAAGVIGEMIARLRPPRPYRAFTKANEFSFOEAEONQRORRKP 480
QY 481 TNORFGNKR 489
Db 481 TNORFGNKR 489

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RESULT 6
US-09-834-721-4
; Sequence 4, Application US/09834721
; Patent No. US20020155551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21123/280169/MAS
; CURRENT APPLICATION NUMBER: US/09/834,721
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: DE 100 26 494.8
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: DE 101 02 823.7
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 489
; TYPE: PRF
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC13032
US-09-834-721-4

Query Match      100.0%; Score 2432; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLSFATLRGISTVDAAKAAAPPSPLAPIDLTHSQVAGVNMIAARIGDILLSSGTSNSD 60
DB      1  MLSFATLRGISTVDAAKAAAPPSPLAPIDLTHSQVAGVNMIAARIGDILLSSGTSNSD 60
QY      61  TKQVRAVTSAYGLYTHVDITNTITITFNIGVERKMPVNVFHVVGKLDTNFSKLEVD 120
DB      61  TKQVRAVTSAYGLYTHVDITNTITITFNIGVERKMPVNVFHVVGKLDTNFSKLEVD 120
QY      121 RLIRSIQAGATPPEVAEKILDELQSPASVGFPAALLGMAMGGAVALVLLGGQVSLIA 180
DB      121 RLIRSIQAGATPPEVAEKILDELQSPASVGFPAALLGMAMGGAVALVLLGGQVSLIA 180
QY      181 FITAFITIAATSEFGKGLPTFFQNVVGGFTATLPASIAVSLAQFGLIKPSQIIASGI 240
DB      181 FITAFITIAATSEFGKGLPTFFQNVVGGFTATLPASIAVSLAQFGLIKPSQIIASGI 240
QY      241 VVLAGLTLVQSLQDGTGATGAVTASARFFETLLFTGIVAGVGIQISEILHVMLEPAME 300
DB      241 VVLAGLTLVQSLQDGTGATGAVTASARFFETLLFTGIVAGVGIQISEILHVMLEPAME 300
QY      301 SAAAPNYSSTFARIIAGVTAAPAVGCVAMSSVITAGLTALMGSAFYVLFVYVLLGVS 360
DB      301 SAAAPNYSSTFARIIAGVTAAPAVGCVAMSSVITAGLTALMGSAFYVLFVYVLLGVS 360
QY      361 AAATAATVGTGGLARRFLIPPLIYVAGITPMLPGAIYRGVYATLNDQTLMGFTNI 420
DB      361 AAATAATVGTGGLARRFLIPPLIYVAGITPMLPGAIYRGVYATLNDQTLMGFTNI 420
QY      421 AVALATASSIAGVVLGEMIAARLRPPRFNPYRAFTKANPFSQEEAEONQORQRKPK 480
DB      421 AVALATASSIAGVVLGEMIAARLRPPRFNPYRAFTKANPFSQEEAEONQORQRKPK 480
QY      481 TNORFGNKR 489
DB      481 TNORFGNKR 489

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; APPLICANT: Sahn, Hermann
; APPLICANT: Thierbach, Georg
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR
; TITLE OF INVENTION: ENZYMAITIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/277066
; CURRENT APPLICATION NUMBER: US/09/783,388
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRF
; ORGANISM: Corynebacterium glutamicum ATCC14752
US-09-783-388-2

Query Match      100.0%; Score 2432; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLSFATLRGISTVDAAKAAAPPSPLAPIDLTHSQVAGVNMIAARIGDILLSSGTSNSD 60
DB      1  MLSFATLRGISTVDAAKAAAPPSPLAPIDLTHSQVAGVNMIAARIGDILLSSGTSNSD 60
QY      61  TKQVRAVTSAYGLYTHVDITNTITITFNIGVERKMPVNVFHVVGKLDTNFSKLEVD 120
DB      61  TKQVRAVTSAYGLYTHVDITNTITITFNIGVERKMPVNVFHVVGKLDTNFSKLEVD 120
QY      121 RLIRSIQAGATPPEVAEKILDELQSPASVGFPAALLGMAMGGAVALVLLGGQVSLIA 180
DB      121 RLIRSIQAGATPPEVAEKILDELQSPASVGFPAALLGMAMGGAVALVLLGGQVSLIA 180
QY      181 FITAFITIAATSEFGKGLPTFFQNVVGGFTATLPASIAVSLAQFGLIKPSQIIASGI 240
DB      181 FITAFITIAATSEFGKGLPTFFQNVVGGFTATLPASIAVSLAQFGLIKPSQIIASGI 240
QY      241 VVLAGLTLVQSLQDGTGATGAVTASARFFETLLFTGIVAGVGIQISEILHVMLEPAME 300
DB      241 VVLAGLTLVQSLQDGTGATGAVTASARFFETLLFTGIVAGVGIQISEILHVMLEPAME 300
QY      301 SAAAPNYSSTFARIIAGVTAAPAVGCVAMSSVITAGLTALMGSAFYVLFVYVLLGVS 360
DB      301 SAAAPNYSSTFARIIAGVTAAPAVGCVAMSSVITAGLTALMGSAFYVLFVYVLLGVS 360
QY      361 AAATAATVGTGGLARRFLIPPLIYVAGITPMLPGAIYRGVYATLNDQTLMGFTNI 420
DB      361 AAATAATVGTGGLARRFLIPPLIYVAGITPMLPGAIYRGVYATLNDQTLMGFTNI 420
QY      421 AVALATASSIAGVVLGEMIAARLRPPRFNPYRAFTKANPFSQEEAEONQORQRKPK 480
DB      421 AVALATASSIAGVVLGEMIAARLRPPRFNPYRAFTKANPFSQEEAEONQORQRKPK 480
QY      481 TNORFGNKR 489
DB      481 TNORFGNKR 489

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RESULT 7
US-09-783-388-2
; Sequence 2, Application US/09783388
; Patent No. US20020168731A1
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Petra
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahn, Hermann
; APPLICANT: Thierbach, Georg
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR
; FILE REFERENCE: 21123/277066
; CURRENT APPLICATION NUMBER: US/09/783,388
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum ATCC13032
US-09-783-388-4

Query Match      100.0%; Score 2432; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSFATLRGRISTVDAAKAAAPPSPLAPIDLTDHSQVAGVMTAAIRIGDILLSSGTSNSD 60
DB 1 MLSFATLRGRISTVDAAKAAAPPSPLAPIDLTDHSQVAGVMTAAIRIGDILLSSGTSNSD 60
QY 61 TKQVRAVTSAYGLYTHVDITLNTTITFTNIGVERMPVNVHVVCKLDTNFSKLSVD 120
DB 61 TKQVRAVTSAYGLYTHVDITLNTTITFTNIGVERMPVNVHVVCKLDTNFSKLSVD 120
QY 121 RLIRSIQAGATPPEVAEKIIDLEQSPASYGFPVALLGMAMGGAVAVLLGGGQVSLIA 180
DB 121 RLIRSIQAGATPPEVAEKIIDLEQSPASYGFPVALLGMAMGGAVAVLLGGGQVSLIA 180
QY 121 RLIRSIQAGATPPEVAEKIIDLEQSPASYGFPVALLGMAMGGAVAVLLGGGQVSLIA 180
DB 121 RLIRSIQAGATPPEVAEKIIDLEQSPASYGFPVALLGMAMGGAVAVLLGGGQVSLIA 180
QY 181 FTAFTIIATTSFLGKKGLPTFPQNVVGFIAFLPASIAVSLALQFGLERKPSQIIASGI 240
DB 181 FTAFTIIATTSFLGKKGLPTFPQNVVGFIAFLPASIAVSLALQFGLERKPSQIIASGI 240
QY 241 VLLAGLTLVQSIQDGTGAPVTASARFFETLLFTGGIVAGVGLIQLSLILHVMLEPAME 300
DB 241 VLLAGLTLVQSIQDGTGAPVTASARFFETLLFTGGIVAGVGLIQLSLILHVMLEPAME 300
QY 301 SAAAPNVSTFARIIAGVTAAPAAFAVGCYAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
DB 301 SAAAPNVSTFARIIAGVTAAPAAFAVGCYAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
QY 361 AAAIAATAVGFOTGLLARRFLIPPLIVAIGITPMLPGAIYRGMTATLNDQTLMGFTNI 420
DB 361 AAAIAATAVGFOTGLLARRFLIPPLIVAIGITPMLPGAIYRGMTATLNDQTLMGFTNI 420
QY 421 AVALATASSLAAGVIGEWIARLRPRPNRPYAFKANEFSFOEAEONORQRPRK 480
DB 421 AVALATASSLAAGVIGEWIARLRPRPNRPYAFKANEFSFOEAEONORQRPRK 480
QY 481 TNORFGNKR 489
DB 481 TNORFGNKR 489

RESULT 9
US-09-951-535-2
; Sequence 2, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELENG, LOTMAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; FILE REFERENCE: 21123/282415/MAS
; CURRENT APPLICATION NUMBER: US/09/951,535
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
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US-09-951-535-2

Query Match      100.0%; Score 2432; DB 10; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSFATLRGRISTVDAAKAAAPPSPLAPIDLTDHSQVAGVMTAAIRIGDILLSSGTSNSD 60
DB 1 MLSFATLRGRISTVDAAKAAAPPSPLAPIDLTDHSQVAGVMTAAIRIGDILLSSGTSNSD 60
QY 61 TKQVRAVTSAYGLYTHVDITLNTTITFTNIGVERMPVNVHVVCKLDTNFSKLSVD 120
DB 61 TKQVRAVTSAYGLYTHVDITLNTTITFTNIGVERMPVNVHVVCKLDTNFSKLSVD 120
QY 121 RLIRSIQAGATPPEVAEKIIDLEQSPASYGFPVALLGMAMGGAVAVLLGGGQVSLIA 180
DB 121 RLIRSIQAGATPPEVAEKIIDLEQSPASYGFPVALLGMAMGGAVAVLLGGGQVSLIA 180
QY 181 FTAFTIIATTSFLGKKGLPTFPQNVVGFIAFLPASIAVSLALQFGLERKPSQIIASGI 240
DB 181 FTAFTIIATTSFLGKKGLPTFPQNVVGFIAFLPASIAVSLALQFGLERKPSQIIASGI 240
QY 241 VLLAGLTLVQSIQDGTGAPVTASARFFETLLFTGGIVAGVGLIQLSLILHVMLEPAME 300
DB 241 VLLAGLTLVQSIQDGTGAPVTASARFFETLLFTGGIVAGVGLIQLSLILHVMLEPAME 300
QY 301 SAAAPNVSTFARIIAGVTAAPAAFAVGCYAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
DB 301 SAAAPNVSTFARIIAGVTAAPAAFAVGCYAEWSSVIIAGLTALMGSAFYLLFVYVLGPVS 360
QY 361 AAAIAATAVGFOTGLLARRFLIPPLIVAIGITPMLPGAIYRGMTATLNDQTLMGFTNI 420
DB 361 AAAIAATAVGFOTGLLARRFLIPPLIVAIGITPMLPGAIYRGMTATLNDQTLMGFTNI 420
QY 421 AVALATASSLAAGVIGEWIARLRPRPNRPYAFKANEFSFOEAEONORQRPRK 480
DB 421 AVALATASSLAAGVIGEWIARLRPRPNRPYAFKANEFSFOEAEONORQRPRK 480
QY 481 TNORFGNKR 489
DB 481 TNORFGNKR 489

RESULT 10
US-09-951-535-4
; Sequence 4, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELENG, LOTMAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; FILE REFERENCE: 21123/282415/MAS
; CURRENT APPLICATION NUMBER: US/09/951,535
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-951-535-4

Query Match      100.0%; Score 2432; DB 10; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLSPATLRGRISTYDAAKAAAPPSPPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 558
; LENGTH: 489
; TYPE: PRN
; ORGANISM: Corynebacterium glutamicum
US-10-627-476-558
Query Match 100.0%; Score 2432; DB 12; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 RLRSIQAGATPPEVAEKILDELEQSPASVGFVALLGMAMMGAVAVLLGGMQVSLIA 180
Db 121 RLRSIQAGATPPEVAEKILDELEQSPASVGFVALLGMAMMGAVAVLLGGMQVSLIA 180
QY 181 FITFTIATTSFEGKGLPFFQNVVGGFTATLPASIAVSLAIOFGLTKPSQIIASGI 240
Db 181 FITFTIATTSFEGKGLPFFQNVVGGFTATLPASIAVSLAIOFGLTKPSQIIASGI 240
QY 241 VVLAAGLTIVOSLDGIGTGAFTASARFFETLLFTGGIVAGVGIGIOSEILHVMPLAME 300
Db 241 VVLAAGLTIVOSLDGIGTGAFTASARFFETLLFTGGIVAGVGIGIOSEILHVMPLAME 300
QY 301 SAAAPNYSSTFARIAGVTAAPAVGCVAMSSVILIAGLTALMGSAFYLLFVYVLGSPVS 360
Db 301 SAAAPNYSSTFARIAGVTAAPAVGCVAMSSVILIAGLTALMGSAFYLLFVYVLGSPVS 360
QY 361 AAAATAATVGTGGILARRFLIPPLIVAGITPMLPGLAIYRGMYATLNDQTLMGFTNI 420
Db 361 AAAATAATVGTGGILARRFLIPPLIVAGITPMLPGLAIYRGMYATLNDQTLMGFTNI 420
QY 421 AVALATASSLAGVVLGEMTARLRPRFPNYPYRAFTANEFSSFOEAEQORQRKPK 480
Db 421 AVALATASSLAGVVLGEMTARLRPRFPNYPYRAFTANEFSSFOEAEQORQRKPK 480
QY 481 TNQRFGNKR 489
Db 481 TNQRFGNKR 489

RESULT 11
US-10-627-476-558
; Sequence 558, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Mark
; APPLICANT: Krieger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habberhauser, Gregor
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CPN
; CURRENT APPLICATION NUMBER: US/10/627.476
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
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QY 1 MLSPATLRGRISTYDAAKAAAPPSPPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 558
; LENGTH: 489
; TYPE: PRN
; ORGANISM: Corynebacterium glutamicum
US-10-627-476-558
Query Match 100.0%; Score 2432; DB 12; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 RLRSIQAGATPPEVAEKILDELEQSPASVGFVALLGMAMMGAVAVLLGGMQVSLIA 180
Db 121 RLRSIQAGATPPEVAEKILDELEQSPASVGFVALLGMAMMGAVAVLLGGMQVSLIA 180
QY 181 FITFTIATTSFEGKGLPFFQNVVGGFTATLPASIAVSLAIOFGLTKPSQIIASGI 240
Db 181 FITFTIATTSFEGKGLPFFQNVVGGFTATLPASIAVSLAIOFGLTKPSQIIASGI 240
QY 241 VVLAAGLTIVOSLDGIGTGAFTASARFFETLLFTGGIVAGVGIGIOSEILHVMPLAME 300
Db 241 VVLAAGLTIVOSLDGIGTGAFTASARFFETLLFTGGIVAGVGIGIOSEILHVMPLAME 300
QY 301 SAAAPNYSSTFARIAGVTAAPAVGCVAMSSVILIAGLTALMGSAFYLLFVYVLGSPVS 360
Db 301 SAAAPNYSSTFARIAGVTAAPAVGCVAMSSVILIAGLTALMGSAFYLLFVYVLGSPVS 360
QY 361 AAAATAATVGTGGILARRFLIPPLIVAGITPMLPGLAIYRGMYATLNDQTLMGFTNI 420
Db 361 AAAATAATVGTGGILARRFLIPPLIVAGITPMLPGLAIYRGMYATLNDQTLMGFTNI 420
QY 421 AVALATASSLAGVVLGEMTARLRPRFPNYPYRAFTANEFSSFOEAEQORQRKPK 480
Db 421 AVALATASSLAGVVLGEMTARLRPRFPNYPYRAFTANEFSSFOEAEQORQRKPK 480
QY 481 TNQRFGNKR 489
Db 481 TNQRFGNKR 489

RESULT 12
US-10-450-055-42
; Sequence 42, Application US/10450055
; Publication No. US20040043953A1
; GENERAL INFORMATION:
; APPLICANT: BASF Aktiengesellschaft
; TITLE OF INVENTION: No. US20040043953A1 genes of Corynebacterium
; FILE REFERENCE: 936 2000
; CURRENT APPLICATION NUMBER: US/10/450.055
; CURRENT FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 42
; LENGTH: 489
; TYPE: PRN
; ORGANISM: Corynebacterium glutamicum
US-10-450-055-42
Query Match 100.0%; Score 2432; DB 12; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSPATLRGRISTYDAAKAAAPPSPPLAPIDLTDSQVAGVNNLAARIGDILLSSGTSNSD 60
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Db 1 MLSPATLRGRISTVDAAKAAAPPSPPLAPIDLTDHSGVAGVNMNLAARIGDILLSSGTSNSD 60
QY 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120
Db 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120
QY 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWNGAVAVLLGGGWQVSLIA 180
Db 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWNGAVAVLLGGGWQVSLIA 180
QY 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLEIKPSQIIASGI 240
Db 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLEIKPSQIIASGI 240
QY 241 VVLAGLTVOSLQDGIITGAPVTASARFFETLLFTGGIVAGVGLGIQISEILHVMLEPAME 300
Db 241 VVLAGLTVOSLQDGIITGAPVTASARFFETLLFTGGIVAGVGLGIQISEILHVMLEPAME 300
QY 301 SAAAPNYSSTFARIIAGGVTAAPFAVGCYAEWSSVITAGLTALMGSAFYVLFVYVLGPVS 360
Db 301 SAAAPNYSSTFARIIAGGVTAAPFAVGCYAEWSSVITAGLTALMGSAFYVLFVYVLGPVS 360
QY 361 AAAIATAVGTGGLARRFLIPLIYAIGITPMLPGAIYRGMYATLNDQTLMGFTNI 420
Db 361 AAAIATAVGTGGLARRFLIPLIYAIGITPMLPGAIYRGMYATLNDQTLMGFTNI 420
QY 421 AVAATATSSIAAGVTLGEMTARLRIRPPRPNPYAFATKANEFSFOEBAEQNRQRKRPK 480
Db 421 AVAATATSSIAAGVTLGEMTARLRIRPPRPNPYAFATKANEFSFOEBAEQNRQRKRPK 480
QY 481 TNORFGNKR 489
Db 481 TNORFGNKR 489

RESULT 13
US-10-224-574-10
; Sequence 10, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
; APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
; APPLICANT: P. Peters- Wendisch
; TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the syt
; TITLE OF INVENTION: L-serin, improved process for the microbial manufacture of L-ser
; TITLE OF INVENTION: genetically modified microorganism suitable for the process.
; FILE REFERENCE: FZJ-9912-PCT
; CURRENT APPLICATION NUMBER: US/10/224,574
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 489
; TYPE: PRT
; ORGANISM: C. glutamicum ATCC 14 752
US-10-224-574-10

Query Match 100.0%; Score 2432; DB 16; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSPTLRGRISTVDAAKAAAPPSPPLAPIDLTDHSGVAGVNMNLAARIGDILLSSGTSNSD 60
Db 1 MLSPTLRGRISTVDAAKAAAPPSPPLAPIDLTDHSGVAGVNMNLAARIGDILLSSGTSNSD 60
QY 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120
Db 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120
QY 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWNGAVAVLLGGGWQVSLIA 180
Db 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWNGAVAVLLGGGWQVSLIA 180

QY 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLEIKPSQIIASGI 240
Db 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLEIKPSQIIASGI 240
QY 241 VVLAGLTVOSLQDGIITGAPVTASARFFETLLFTGGIVAGVGLGIQISEILHVMLEPAME 300
Db 241 VVLAGLTVOSLQDGIITGAPVTASARFFETLLFTGGIVAGVGLGIQISEILHVMLEPAME 300
QY 301 SAAAPNYSSTFARIIAGGVTAAPFAVGCYAEWSSVITAGLTALMGSAFYVLFVYVLGPVS 360
Db 301 SAAAPNYSSTFARIIAGGVTAAPFAVGCYAEWSSVITAGLTALMGSAFYVLFVYVLGPVS 360
QY 361 AAAIATAVGTGGLARRFLIPLIYAIGITPMLPGAIYRGMYATLNDQTLMGFTNI 420
Db 361 AAAIATAVGTGGLARRFLIPLIYAIGITPMLPGAIYRGMYATLNDQTLMGFTNI 420
QY 421 AVAATATSSIAAGVTLGEMTARLRIRPPRPNPYAFATKANEFSFOEBAEQNRQRKRPK 480
Db 421 AVAATATSSIAAGVTLGEMTARLRIRPPRPNPYAFATKANEFSFOEBAEQNRQRKRPK 480
QY 481 TNORFGNKR 489
Db 481 TNORFGNKR 489

RESULT 14
US-10-224-574-12
; Sequence 12, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
; APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
; APPLICANT: P. Peters- Wendisch
; TITLE OF INVENTION: Nucleotide sequences coding for proteins participating in the syt
; TITLE OF INVENTION: L-serin, improved process for the microbial manufacture of L-ser
; TITLE OF INVENTION: genetically modified microorganism suitable for the process.
; FILE REFERENCE: FZJ-9912-PCT
; CURRENT APPLICATION NUMBER: US/10/224,574
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 489
; TYPE: PRT
; ORGANISM: C. glutamicum ATCC 13 032
US-10-224-574-12

Query Match 100.0%; Score 2432; DB 16; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.5e-214;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSPTLRGRISTVDAAKAAAPPSPPLAPIDLTDHSGVAGVNMNLAARIGDILLSSGTSNSD 60
Db 1 MLSPTLRGRISTVDAAKAAAPPSPPLAPIDLTDHSGVAGVNMNLAARIGDILLSSGTSNSD 60
QY 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120
Db 61 TKVQRAVTSAYGLYYTHVDITLNTITITFTNIGVERKMPVNVFHVVGKLDITNFSKLSVD 120
QY 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWNGAVAVLLGGGWQVSLIA 180
Db 121 RLIRSIQAGATPEPVAEKLIDELQSPASYSYGPVALLGMAWNGAVAVLLGGGWQVSLIA 180
QY 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLEIKPSQIIASGI 240
Db 181 FITAFITIAATTSFLGKKGLPTFFQNVVGGFIATLPASIAVSLALQFGLEIKPSQIIASGI 240
QY 241 VVLAGLTVOSLQDGIITGAPVTASARFFETLLFTGGIVAGVGLGIQISEILHVMLEPAME 300
Db 241 VVLAGLTVOSLQDGIITGAPVTASARFFETLLFTGGIVAGVGLGIQISEILHVMLEPAME 300
QY 301 SAAAPNYSSTFARIIAGGVTAAPFAVGCYAEWSSVITAGLTALMGSAFYVLFVYVLGPVS 360
Db 301 SAAAPNYSSTFARIIAGGVTAAPFAVGCYAEWSSVITAGLTALMGSAFYVLFVYVLGPVS 360

QY 361 AAAIATAVGFTGGLARRFLIPPLIVAIAGITPMDPGAIYRGWYATINDOTLMGFTNI 420
 DB 361 AAAIATAVGFTGGLARRFLIPPLIVAIAGITPMDPGAIYRGWYATINDOTLMGFTNI 420
 QY 421 AVALATASSIAGVVGEMTARLRPRPNPYRAFTKNEFSFOEAEQNRQRKRPK 480
 DB 421 AVALATASSIAGVVGEMTARLRPRPNPYRAFTKNEFSFOEAEQNRQRKRPK 480
 QY 481 TNORFGNKR 489
 DB 481 TNORFGNKR 489

RESULT 15

US-09-738-626-6384
 ; Sequence 6384, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIHO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738, 626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 6384
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-6384

Query Match 100.0%; Score 2432; DB 9; Length 501;
 Best Local Similarity 100.0%; Pred. No. 4.7e-214;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSFATLGRISTVDAAKAPPPSLAPIDLTDHSQVAGVMMLAARIGDILSSGTSNSD 60
 DB 13 MMSFATLGRISTVDAAKAPPPSLAPIDLTDHSQVAGVMMLAARIGDILSSGTSNSD 72
 QY 61 TKQVRAVTSAYGLYTHVDITLNTITFTNIGVERKMPVNFHVVGKLDINFSKLSVD 120
 DB 73 TKQVRAVTSAYGLYTHVDITLNTITFTNIGVERKMPVNFHVVGKLDINFSKLSVD 132
 QY 121 RLIRSIQAGATPEVAEKILDELQSPASGYGFPVALIGWAMMGAVAVLLGGWQVSLIA 180
 DB 133 RLIRSIQAGATPEVAEKILDELQSPASGYGFPVALIGWAMMGAVAVLLGGWQVSLIA 192
 QY 181 FITAFIIATTSFLGKGLPTFFQNVVGGFIATLPASIVSLALQGLEIKPSQIIASGI 240
 DB 193 FITAFIIATTSFLGKGLPTFFQNVVGGFIATLPASIVSLALQGLEIKPSQIIASGI 252
 QY 241 VVLLAGLTVGSIGDGTAPVTASARFETILLFTGGIYAGVGLGIQISEIILHVMIPAME 300
 DB 253 VVLLAGLTVGSIGDGTAPVTASARFETILLFTGGIYAGVGLGIQISEIILHVMIPAME 312
 QY 301 SAAAPNYSSTFARIAGVTAAAFVAGCYAEMSSVLIAGLTALMSGAPFYLLFVVYLG PVS 360

DB 313 SAAAPNYSSTFARIAGVTAAAFVAGCYAEMSSVLIAGLTALMSGAPFYLLFVVYLG PVS 372
 QY 361 AAAIATAVGFTGGLARRFLIPPLIVAIAGITPMDPGAIYRGWYATINDOTLMGFTNI 420
 DB 373 AAAIATAVGFTGGLARRFLIPPLIVAIAGITPMDPGAIYRGWYATINDOTLMGFTNI 432
 QY 421 AVALATASSIAGVVGEMTARLRPRPNPYRAFTKNEFSFOEAEQNRQRKRPK 480
 DB 433 AVALATASSIAGVVGEMTARLRPRPNPYRAFTKNEFSFOEAEQNRQRKRPK 492
 QY 481 TNORFGNKR 489
 DB 493 TNORFGNKR 501

Search completed: July 31, 2004, 10:26:44
 Job time : 1070 secs